Aay70913 Human ec Aay70890 Protein

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                                                                                       September 21, 2005, 11:47:33 ; Search time 89 Seconds (without alignments) 2216.267 Million cell updates/sec
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                                                             OM protein - protein search, using
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Total number of hits satisfying chosen parameters:

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Database

geneseqp1990s: \*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Length DB ID	:	2 AAW04264 Human	3 AAY70910 Aay70910 Human	3 AAY70887 Human	510 4 AAB71917 Aab71917 Human CD3	7 ADJ57262 Adj57262	8 ADL24295 Adl24295	510 8 ADQ99453 Auman CD3	8 ADR69210				8 ADR87821 Adr87821		8 ADK60722 Adk60722	8 ADP73345 Adp73345	7 ADN95839 Adn95839	8 ADK60221 Adk60221	8 ADK60522 Adk60522	8 ADP73145 Adp73145	8 AB084672 Abo84672	ABM83376 Abm83376		000000000000000000000000000000000000000
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Human soluble CD39 protein
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N-PSDB; AAT33966
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ATP diphosphohydrolaes; transgenic animal; pig; porcine; graft; donor; transplantation; endothelial cell; prosthetic device; platelet aggregation; inhibition; intravascular.
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12-FEB-1996;
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therapy of inflammatory or immunological stimulation of platelet sgation - using CD39 protein with ATP di.phospho.hydrolase activity, al for preventing or alleviating thrombotic condition in mammalian
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100.0%; Pred. No. 5.2e-262;
ive 0; Mismatches 0;
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Sequence 510 AA;

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The present sequence is the human soluble CD39 protein, a cell surface molecule, having apyrase activity. It is derived from a human B cell line CDMA library, referred to as MP-1. Soluble CD39 is constructed by removing the N- and C-terminal transmembrane domains. It retains the capacity to metabolise ATP and ADP at relevant concentrations and the ability to block and reverse ADP-induced platelet activation and cervariant in an angle and the ability to block and reverse ADP-induced platelet activation and cervariant in an angle angines are useful for thibiting angiogenesis. It is useful for the treatment of unstable angina, myccardial infartion, stroke, coronary artery disease or injury, atherosclerosis, peripheral vaccular occlusion, precelampsia, embolism, platelet-associated ischaemia, thrombotic disorders including lung, coronary and cerebral ischaemia, thrombotic disorders including coronary, peripheral and creabral artery thrombosis, intracardiac and venous thrombosis, coogulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, steocclusion, steocclusion, steocclusion, steocclusion, steocclusion, attored.
             Soluble CD39; human, apyrase activity; platelet activation; inhibitor; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombus formation; occlusion; stenosis; restenosis; angiogenesis; antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New soluble CD39 polypeptides having apyrase activity, useful for inhibiting angiogenesis and treating unstable angina, myocardial infarction, stroke, coronary artery disease or injury.
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//note= "Asn is N-glycosylated" 477. .499
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192. .294
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06-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; presclampsia; embolism; platelet-associated ischaemic disorder; lung ischaemia; thrombolytic; cerebral ischaemia; thrombotic disorder; lung ischaemia; thrombosis; cerebral artery thrombosis; intracardiac thrombosis; renous thrombosis; peripheral artery thrombosis; coagulopathy; deep venous thrombosis; PE; pulmonary embolism; transient ischaemic attack; thrombosis; DYT; PE; pulmonary embolism; transient ischaemic attack; thrombus formation; cecclusion; secolusion; stenosis; resteanosis; antianginal; cardiant; cerebroprotective; antianteriosclerotic; vasotropic; anticoagulant;
                                                                                                                                                              SLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQ
                                                                                            1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALLAVGLTQNKALPENVKYGIVLDAGSSHT
                                                                                                                                                                                                                                                                                 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFR
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                                                                     1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALLAVGLTQNKALPENVKYGIVLDAGSSHT
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                                      Gaps
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   510;
   Length
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Score 2698; DB 3;
Pred. No. 5.2e-262;
; Mismatches 0;
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/labbl= Transmembrane_domain
73. .75
/note= "Asn is N-glycosylated"
227. .229
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                                    ö
 100.0%;
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                                  Matches 510; Conservative
 Query Match
Best Local Similarity
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Sequence 510 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
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                                                                                                                                                                                                                                                                                                                                                                                          mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD39
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                                            /note= "Asn is N-glycosylated"
371. .373
                                             371. .373
/note= "Asn is N-glycosylated"
457. .459
          292. .294
/note= "Asn is N-glycosylated"
334. .336
                                                                                   457. .459
/note= "Asn is N-glycosylated"
"Asn is N-glycosylated"
                                                                                                           477. 499
/label= Transmembrane_domain
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RES FOUND INC.
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98US-0107466P.
99US-0149010P.
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es 510; Conservative
  note=
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(CORR ) CORNELL
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                                                                                                                                                  WO200023094-A2
           Modified-site
                                   Modified-site
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06-NOV-1998;
13-AUG-1999;
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The present sequence is the human CD39 polypeptide. The present sequence or its active fragment may be administered to treat or prevent stroke in a subject susceptible to intracranial haemorrhaging or an ischaemic disorder. The CD39 polypeptide inhibits ADP-mediated platelet aggregation or leukocyte accumulation and/or ATP by increasing ADP catabolism to the subject. It is useful for treating or preventing stroke, thrombotic disorders and ischaemic disorders such as peripheral vascular disorder, pulmonary embolus, venous thrombosis, myocardial infarction, transient ischaemic attack, unstable angina, reversible ischaemic neurological deficit and sickle cell anaemia. It is also useful for treating or preventing a stroke disorder in a subject undergoing heart surgery, lung surgery, spinal surgery, brain surgery, vascular surgery, abdominal surgery, or organ transplantation surgery
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                                                       LYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP 300
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                                                                                                                                                                                 CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGAF
                                                                                                                                                                                                                   SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL
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SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
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                 19-FEB-2003; 2003WO-US004845
                                  20-FEB-2002; 2002US-0358303P
                                                                          Elmaleh DR, Robson SC,
                                                  (GEHO ) GEN HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                  Sequence 510 AA;
28-AUG-2003
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nes 510;
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                                                    MEDTKESNVKTFCSKNILAILGFSSIIAVIALLAVGLTQNKALPENVKYGIVLDAGSSHT
                                                                                   LYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP
                                                                                                                                                                                         LYGKDYNVYTHSFLCYGKDQALMQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP
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                                        1 MEDIKESNVKTFCSKNILAILGFSSIIAVIALLAVGLTQNKALPENVKYGIVLDAGSSHT
                                                                                                           HQETPVYLGATAGMRLLRMESEBLADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWI
                                                                                                                                             TINYLLGKFSQKTRWFSIVPYETINNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFR
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        Length
                        Indels
       Score 2698; DB 4;
Pred. No. 5.2e-262;
Mismatches 0;
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      100.08;
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/note = ACR1
125. .135
/note = ACR2
171. .183
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               1 Similarity 100.
510; Conservative
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The invention relates to a conjugate (I) comprising an enzyme and a biodegradable polymer, where (i) enzymatic activity of the enzyme is biodegradable polymer, to that of the enzyme in the absence of the biodegradable polymer, or (ii) the half life of the enzyme is longer than that of the enzyme in the absence of the polymer. The enzymatic activity (i) is at least 10 (preferably at least 100) times higher in the presence of the polymer. The enzyme is a multimeric, soluble and/or extracellular enzyme, preferably an apyrase, especially a soluble form of CD39 and catalyzes hydrolysis of nucleoside diphosphate. The conjugate can be used to treat diseases relating to abnormal levels of extracellular nucleotides or abnormal aggregation of platelets, particularly cardiovascular disease, cancer, espsis or a disease related to graft transplant. (I) is also used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for treating coronary artery disease or injury following myocardial infarction, unstable angina, atherosclerosis, pre-eclampsia, embolism, platelet associated ischaemic disorders including lung, coronary and cerebral ischaemia, reocclusion following thrombosis, thrombotic disorders, and thrombosis and coagulopathies associated with exposure is foreign or injured tissue surface, in combination with angioplasty, carotid endarterectomy, anastomosis of vascular grafts and chronic cardiovascular devices. The present sequence represents a human CD39
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                                                                                                            New enzyme polymer conjugate used for treating abnormal levels of extracellular nucleotides or platelet aggregation, graft transplant, cardiovascular disease, cancer and sepsis.
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WPI; 2003-778966/
N-PSDB; ADJ57261
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                                                                                                                                                                                                                                                                             CD39-like protein; gene mapping; molecular weight marker; food supplement; anti-thrombotic; anti-tissue graft rejection agent; ATP neurotransmission; ecto-ATPase activity; nucleotide triphosphatase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New CD-39-like polypeptides and polynucleotides, useful in chromosome gene mapping, as molecular weight markers, as food supplements, or as anti-thrombotic or anti-tissue graft rejection agents.
                                                                  181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFR
                                                                                                                                                         CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGAF
                                                                                                                                                                        CTKRFEMTLPPQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGAF
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                                                                                                      LYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP
             HQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPPDFQGARIITGQEEGAYGWI
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169. .191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQ 120
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SLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFL 480
                                                         SLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a method of treating cardiovascular disease in a subject, comprising administering an IL-17, IL-18, 4-1BB, CD30 or OX40 antagonist. The IL-17, IL-18, 4-1BB, CD30 or OX40 antagonists are useful for treating cardiovascular disorders, e.g. (chronic immune) myocarditis, congestive heart failure, aneurysms, angina, embolism, restenosis, ischaemia or thrombocytopenic purpura. The present sequence is a polypeptide used in the exemplification of the
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                                                                                                                                                                                                                                                                                            cardiovascular disease; IL-17; interleukin; IL-18; 4-1BB; CD30; OX40;
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                                                  The invention relates to novel CD39-like polypeptides (CD39-like
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                                                                                                                                                                                                                                                                                                                                                               Length 510;
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100.0%; Pred. No. 5.2e-262;
ive 0; Mismatches 0;
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                  8; 104pp; English.
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Matches 510; Conservative
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              Example, Fig
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The present invention relates to CD39-like polypeptide and its encoding polymucleotide. The invention is useful for preventing, treating or ameliorating autoimmune deficiency disorders including connective tissue disease, multiple sclerosis, specimic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent disbetes mellitus mysathenia gravis, graft-versus-host disease or autoimmune inflammatory eye disease, myeloid or lymphoid call deficiencies, periodontal diseases and other tooth repair processes, inflammatory conditions including inflammatory bowel disease and Crohn's disease, leukaemias and nervous system city inflammatory conditions including inflammatory bowel disease and Crohn's disease, leukaemias and nervous system inhibiting platelet aggregation, food supplement, anti-tissue graft rejection agents, for regulating neurotransmission by ATP in smooth sequence is a human CD39 protein. Note: This sequence is stated to be the same as that shown as SEQ ID 13 in sequence listing, however these
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autoimmune pulmonary inflammation, Guillain-Barre syndrome; autoimmune thyroiditis; insulin dependent diabetes mellitus; manatura autoimmune thyroiditis; insulin dependent diabetes mellitus; myasthenia gravis; graft-versus-host disease; disease; autoimmune inflammatory eye disease; allergic disorder; asthma; respiratory disease; myeloid or lymphoid cell deficiency; periodontal disease; tooth repair process; inflammatory bowel disease; crohn's disease; leukaemia; nervous system disorder; anticoagulant; food supplement; anti-tissue graft rejection; ATP neurotransmission;
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100.0%; Pred. No. 5.2e-262;
ive 0; Mismatches 0;
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/note= "Apyrase region
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207. .228
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                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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Matches 510;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   systemic lupus erythematosus;
human immunodeficiency virus-associated myelopathy;
transverse myelopathy; nutritional disorder; vitamin B12 deficiency;
folic acid deficiency; Wernicke disease; tobacco-alcohol amblyopia;
Marchiafava-Bignami disease; haemostatic activity; thrombolytic activity;
nutritional supplement; ecto-ATPase activity; cytostatic; immunotherapy;
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                   SLYIYKWPAEKENDIGVVHQVEECRVKGPGISKFVQKVNBIGIYLTDCMERAREVIPRSQ 120
                                                               HOETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWI 180
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/note= "A-
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uncleotide triphosphatase; NTPase) and their encoding polynucleotides.

The invention is useful in treating cancer, leukaemia and related
disorders such as acute lymphocytic leukaemia, acute myelocytic leukaemia

CC and chronic leukaemia, autoimmune disorders such as multiple sclerosis,
crematoid arthritis, Guillain-Barre syndrome, insulin dependent diabetes

CC rhematoid arthritis, Guillain-Barre syndrome, insulin dependent diabetes

CC disorders such as atthma, respiratory disorders, inflammatory disorders

CC disorders such as atthma, respiratory disorders, inflammatory disorders

CC chon's disease, central and peripheral nervous system disorders such as

CC chon's disease, central and peripheral nervous system disorders such as

CC crohn's disease, human immunodeficiency virus associated

CC systemic lupus erythematosus, human immunodeficiency virus associated

CC wyelopathy and transverse myelopathy and nutritional disorders such as

CC alcohol amblyopia and Marchiafava-Bignami disease. The invention also has

CC alcohol amblyopia and marchiafava-Bignami disease. The invention also has

CC and modulates ecto-ATPase activity. The invention acts as a cytostatic

cagent and is useful in immunotherapy. The present sequence is human CD39

CD protein. Note: This sequence is described in the specification as being

CC sequence listing, however the two sequences are different.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention provides novel CD39-like polypeptides (CD39-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALLAVGLTQNKALPENVKYGIVLDAGSSHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Fig 8; 102pp; English.
                                                                     29-JAN-1999; 99US-00240639.
13-JUL-2001; 2001US-00905589.
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Best Local Similarity 100.
Matches 510; Conservative
                                                                                                                                                                                                                                                                               Chadwick BP, Frischauf
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                                                                                                                                                                                                 NUVE-) NUVELO INC
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                                                                                                                                                                                                                                                                                                                                                                                                  GENBANK; S73813.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancerous cells.
27-MAR-2002;
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Length 510; IndelB 120 120 180

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SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
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               and for identifying compounds that can be utilised for modulating ecto-
Arpase activity. The invention is useful for preventing, treating or
ameliorating a medical condition, e.g. multiple actarosis, rheumatoid
arthritis, autoimmune thyroiditis, diabetes mellitus, myasthenia gravis,
autoimmune inflammatory eye disease, osteoporosis, osteoarthritis,
Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,
leukaemia or nervous system disorders and in gene therapy. The present
sequence is the human CD39 protein. Note: This sequence is stated to be
the same as that shown as SEQ ID 13 in sequence listing, however these
     markers, and as food supplements and for modulating ecto-ATPase activity
                                                                                                                                                                                                                                                                                                                                                                                       SLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQ
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                                                                                                                                                                                                                              100.0%; Score 2698; DB 8;
100.0%; Pred. No. 5.2e-262;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                            510; Conservative
                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                               sequences differ.
                                                                                                                                                                                               Sequence 510 AA;
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CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGAF 360
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                                                                                                                                                                                                                                                                                                                                                                                                      CD39-like protein; gene mapping; food supplement; ecto-ATPase activity; gene therapy; multiple sclerosis; rheumatoid arthritis; autoimmune thyroiditis; diabetes mellitus; myasthenia gravis; autoimmune throiditis; diabetes mellitus; myasthenia gravis; autoimmune inflammatory eye disease; osteoporosis; osteoarthritis; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; leukaemia; nervous system disorder; neuroprotective; antiarthritic; antirheumatic; antithyroid; immunosuppressive; antidiabetic; muscular-gen; ophthalmological; osteopathic; nootropic; antiparkinsonian; cytostatic; human; CD39 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a CD39-like polypeptides and the encoding polymucleotides. The CD39L4 polymucleotide is useful as hybridisation probes, as primers for PCR, for chromosome or gene mapping, in the recombinant production of protein, and in generation of antisense DNA or RNA. The protein of the invention is used as molecular weight
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                                                SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL
                                                                                              SLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFL
                               SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated CD3914 polynucleotide, useful for preventing, treating, ameliorating multiple sclerosis, rheumatoid arthritis, diabetes, osteoporosis, Alzheimer's disease, amyotrophic lateral sclerosis, or
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124. .14
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169. .19
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New isolated CD39L3 polypeptide and polynucleotide, useful for diagnosing, preventing or treating HIV, hepatitis, multiple sclerosis, systemic lupus erythematosus, arthritis, diabetes and asthma.
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TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFR
                                                                                                    241 LYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNNVSDLYKTP
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                                                                                                                                                                                                                                                                                                                                                                361 SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV infection, hepatitis, multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; systemic lupus erythematosus; rheumatoid arthritis; guillain-Barre syndrome; thyroiditis; diabetes; myasthenia gravis; graft-versus-host disease; GHVD; asthma; human; enzyme; CD39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; CD39-like nucleotide-triphosphatase; NTPase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Apyrase region (ACR) III"
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/note= "Apyrase region (ACR)
125. .142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481 MVLFSLVLFTVAIIGLLIFHKPSYFWKDMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . .228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human CD39 protein #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-623544/60.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid comprising at least 10 in the specification, or its complement. The nucleic acids encode cancerassociated proteins. Also included are an expression vector comprising the isolated nucleic acid cited above, a host cell comprising the above recombinant nucleic acid cited above, a host cell comprising the above comprising at least onclevide acid comprising at least one probe comprising at least 10 contiguous nucleotides of any of the above comprising at least 10 contiguous nucleotides of any of the above comprising at least 10 contiguous nucleotides of any of the above an open reading frame of a CA sequence selected from any of the 35 complement), an isolated antibody, (or its antigen binding fragment) that on open reading frame of a CA sequence selected from any of the 35 complement), an isolated antibody, (or its antigen binding fragment) that binds to the above polypeptide, a hybridoma that produces the above comprising the above polypeptide, a hybridoma that produces the above contribudy and a pharmaceutical excipient, a kit for detecting cancer cells (comprising the antibody, a pharmaceutical composition comprising the above contribudy and pharmaceutical excipient, a kit for detecting cancer cells (comprising the antibody of cancer of cancer cells in an individual, a method for inhibiting a therapeutic agent to cancer cells in an individual, an electronic library comprising the above for antividual, an electronic library comprising the above for antividual, and the expression of a polypeptide for inhibiting the above concerning content activity of a CA protein (CAP), methods for detecting cancer associated with expression of a polypeptide for inhibiting the expression of a method for treating cancers and a method for inhibiting the expression of cancer cancer. The present sequence is a human CAP protein sequence of a nucleic or pell in a lest for this patent did not form agents that inhibiting described and a method for the present sequence as a nucleic or pell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLYIXWWPAEKENDTGVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated cancer-associated polynucleotides and polypeptides useful for diagnosing, preventing or treating cancers, especially lymphoma and leukemia, or in screening for agents that modulate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                         Malandro MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             claim 18; seqid 698; 310pp; English
                                                , 2003US-00367094.
; 2003US-0038838.
; 2003US-00417375.
; 2003US-00461862.
; 2003US-0063431.
  17-FEB-2004; 2004WO-US004730
                                                                                                                                                                                                                                         SAGR-) SAGRES DISCOVERY INC
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Matches 510; Conservative
                                                                                                                                                                                                                                                                                       Morris DW,
                                                                                                                                                                                                                                                                                                                                          WPI; 2004-652914/63.
N-PSDB; ABD32958.
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                                                                                                                                                          15-SEP-2003;
15-DEC-2003;
                                                                                                      5-APR-2003;
                                                                                                                                    13-JUN-2003;
                                                                                                                                                                                                                                                                                         Morris DW,
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241 LYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP 300
      retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis;
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                                                                                                                                                          Homo sapiens.
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                                                                               triphosphateae; NTPase) and their corresponding polynucleotides. The invention also relates to a method for making CD3D proteins. The methods and compositions of the invention are useful for the diagnosis. The methods prevention and/or treatment of diseases or conditions associated with infection, hepatitis, multiple sclerosis, systemic lupus erythmatosus, rheumatoid arthritis, multiple sclerosis, systemic lupus erythmatosus, rheumatoid arthritis, duillain Barre syndrome, thyroiditis, diabetes, present sequence is the human CD39 protein. Note: This sequence is described in the specification as being the same as the human CD39 protein represented in SEO ID NO: 13 of the sequence listing, however the
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                                                               invention relates to CD39-like polypeptides (CD39-like nucleotide
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                                                                                                                                                                                                                                                                                                                                sequences are different
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The invention relates to a novel pharmaceutical composition active on angiogenesis comprising an endothelial cell nucleic acid whose expression is induced by an angiogenic factor and inhibited by an angiostatic agent or its complement or fragment, a polypeptide sequence encoded by the nucleic acid or its fragment, a molecule capable of inhibiting expression of the nucleic acid or a molecule which binds to the polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Compositions for diagnosing, prognosing and treating angiogenic disorders including tumor vascularization and heart disease, comprise nucleic acid or polypeptide differentially expressed in angiogenesis.
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ovary hyperstimulation; psoriasis; endometriosis; restenosis; angioplasty; cicatrisation; peripheral vascular disease; hypertension; vascular inflammation; Raynaud's disease; aneurism; thrombophlebitis; ischemia; angina; myocardial infarction; chronic heart disease;
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ive 0; Mismatches 0;
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                                                                                                                                                                Compositions containing nucleic acid or polypeptide differentially expressed in angiogenesis are useful to diagnose, prognose and treat angiogenic disorders including tumor vascularization and heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                        vasotropic, antirheumatic, antiarthritic, hypotensive, antianginal, antinflammatory, cardiant, angiogenesis inhibitor; gene therapy; angiogenesis, endochelial cell, diagnosis, tumor vascullarization; retinopathy; rheumatoid arthritis; Crohn's disease, atheroselerosis; ovary hyperstimulation; psoriasis; endometriosis, restenosis; angioplasty; cicatrisation; peripheral vascular disease, hypertension; vascular inflammation; Raymaud's disease; aneurism; thrombophlebitis; ischemia, angina; myocardial infarction; chronic heart disease; cardiac congestion; macular degeneration; osteoporosis.
                                                                  CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGAF
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Ltd.
Compugen
- 2005
:) 1993
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right

OM protein - protein search, using sw model

0 ; Search time 25 Seconds (without alignments) 1962.822 Million cell updates/sec September 21, 2005, 15:52:40 Run on:

Perfect score:

US-09-807-660C-2
2698
1 MEDTKESNVKTFCSKNILAI.....VAIIGLLIFHKPSYFWKDMV Sequence:

510

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283416 segs, 96216763 residues

283416

length: 0 length: 2000000000 seq seq 88 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
1: pir3:\*
: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		lymphoid cell acti			cal	_	probable nucleosid	hypothetical prote	w	hypothetical prote	probable guanosine	nucleoside triphos	hypothetical prote	аругаве (ЕС 3.6.1.	hypothetical prote	guanosine-diphosph	nucleoside-triphos	C4-dicarboxylage-b	beta-galactosidase	hypothetical prote		hypothetical prote	Mg2+ transporter h	hypothetical prote	>	TipC protein - sli	hypothetical prote	$\neg$	hypothetical prote	
SUMMARIES	DB ID	2 I56242	2 D86276	2 E86276	2 S50463	T4085		T3414							2 T23508									T2151	A7236	T1741	E	B4396	B9019	AB141
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de	Query Match	100.0	19.0	17.4	16.9	16.1	15.6	15.3	14.9	14.7	14.1	13.9	13.0	12.7	12.3	•	6.3	5.4	4.5	4.2	4.0			3.8	3.7	•	٠	3.7	•	3.7
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p60-related protei hypothetical prote	hypothetical prote hypothetical prote hypothetical prote	hypothetical prote penicillin-binding probable histidine	hypothetical prote chitin synthase (E probable fimbrial	myosin I beta - bu DNA-directed DNA p	probable permease probable permease hypothetical prote
AB1695 D86247	B84532 B89985 T05213	A96738 A97743 T03774	E71086 JC2314 B85725	I51173 D86890	531228 F86075 F89770
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98.5	98.5 98.5 98	97.5 97.5 97	97 96.5 96	96	9 9 9 9 0 0 9 0 0 9 0 0
30	3 B B	35 37	3 8 8 4 0 8	444	444

## ALIGNMENTS

lymphoid cell activation antigen - human C; Species: Homo sapiens (man) C; Species: O-20ul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004 C; Accession: I56242 Fanslow, W.C.; J. Immunol. 153, 3574-3583, 1994 J. Immunol. 153, 3574-3583, I56242 J. Juli: PMID:95015846; PMID:7930580 J. Juli: Jecession: I56242 J. Juli: Jecession: Jecession: I56242 J. Juli: Jecession: Jecession: I56242 J. Juli: Jecession: Jec

Length 510; Query Match

ö 9 9 1 MEDIKESNVKTFCSKNILAILGFSSIIAVIALLAVGLTQNKALPENVKYGIVLDAGSSHT 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALLAVGLIONKALPENVKYGIVLDAGSSHT Gaps ö Indels 100.0%; Score 2698; DB 2; 100.0%; Pred. No. 4.1e-206; ive 0; Mismatches 0; Best Local Similarity 100. Matches 510; Conservative 셤 ò

120 120 SLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQ SLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQ 61 61 g ð

HQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWI 180 180 121 HQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWI 121 ઠે g

240 240 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFR 181 g ઠે

300 300 LYGKDYNVYTHSFLCYGKDQALMQKLAKDIQVASNEILKBPCFHPGYKKVVNVSDLYKTP 241 ઠે 셤

360 360 CTKR FEMTLP FOOFEI OGIGNY QOCHOSILELFNTSY CPYSOCAFNGIFL PPLOGDFGAF 301 g ò

420 361 SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCPSGTYIL a ઠે ò

SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL

361

420

480 480 SLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFL SLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFL 421 421 g

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Query Match 17.4*
Best Local Similarity 31.2*
Matches 123; Conservative
                                                                                                                                                                                                                                      A,Accession: E86276
A,Status: preliminary
A,Molecule type: DNA
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                                                                                                                               Dybotherical protein F7A19.34 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 (CACCESSION: D26276 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L. (Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. (A.) Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Reference number: A86141; MUID:21016719; PMID:11130712 Arabidopsis. A; Residues: 1-483 <STO> A; G.; Fraser, C.M.; Wu, D.; Yu, G.; Fraser, C.M.; Wull Arabidopsis. A; Residues: 1-483 <STO> A; Genetics: A; Map position: 1 C; Superfamily: nucleoside triphosphatase chromatin-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 QETPVYLGATAGMRLLRMESEELADRVLDVVERSL--SNYPFDFQGARIITGQEEGAYGW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 ITINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQF 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLYKTPCTKRFEMTLPFQQFEIQG----IGNYQQCHQSILELF--NTSYCPYSQCAFNGI 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 KWPAEKEN---DTGVVHQVEECRVK-GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 RLYGK-DYNVYTHSFLCYGKDOALWOKLAKDIQVASNE----ILRDPCFHPGYKKVVNVS 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -IYDTN-SKNYSSGFLADESKLKGSLQAAGNFSKCRSATFALLKEGKENCLYEHCSIGST 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 SKSLI-LLVVVSVTITLGLLLYVFNSNSVISSGSLLSRRCKLRYSVLIDAGSSGTRVHVF 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 SKNILAILGFSSIIAVIALLAVGLTQNKALPE-----NVKYGIVLDAGSSHTSLYIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FTPDLQGSFLATASFYYTAKFFEL-BEKGWLSELIPAGKRYCGEEWSKLILEYPTTDEEY
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LRGYCFSAAYTISMLHDSLGIALDD-ESITYASK----AGEKHIPLDWALG 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                   481 MVLFSLVLFTVAIIGLLIFHKPSYFWKDMV 510
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Matches 142; Conservative
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E86276 hypothetical protein F14L17.1 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)

RESULT 3

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R;Theologia, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, R;Theologia, A.; Ecker, J.R.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.K.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, II, Artile: Sequence and analysis of chromosome I of the plant Arabidopsis.
A;Title: Sequence number: A86141; WUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypochetical protein YER005w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Spate: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
C;Accession: S50463
R;Dietrich, F.S.
Subditted to the EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae cosmids 9537, 9581, 9495, 9867, and lambda cA;Reference number: S50433
A;Molecule type: DNA
A;Residues: 1-630 < DIE>
A;Coss.references: UNIFROT:P40009; EMBL:U18778; NID:g603592; PID:g603597; GSPDB:GN00005, A;Coss.references: Unifron Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-405 <STO>
A;Cross_references: UNIPROT:Q9M9T7; GB:AE005172; NID:g7262666; PIDN:AAF43924.1; GSPDB:GNC
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 LDVVERSLSNYPFDFQG--ARIITGQEEGAYGWITINYLLGKFSQKTRWFSIVPYETNNQ 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 WQKLAKDIQVASNE-ILRDPCFHPGYKKVVNVSDLYKTPCTK------RFEMTLPF 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 FGL-GEK---EWLSEMILAGKRFCGEEWSKLKEKYPTTKDKYLHRYCFSSAYIISMLHDS 353
Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 LDVTRRVLRSSGFKFQDEWATVISGTDEGIYAWVVANHALGSLG-------GDPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 ---QVQAAGDFTKCRSATLAMLQEGKENCAYKHCSIGSTFTPNIQGSFLATENFFHTSKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 PGISKFVQKVNBIGIYLTDCMERARBVIPRSQHQETPVYLGATAGMRLLRMESEELADRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 ETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGK-DYNVYTHSFLCYGKDQA---L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312 QQFEIQGIGNYQQCHQSILELF -- NTSYCPYSQCAFNGIFLPPLQGDFGAFSAFYFVMKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 PGLSSYADNPEGASVSVTKLVEFAKGRIPKGKLKKSDIRLMATAGMRLLDVPVQE---QI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 469.5; DB 2;
; Pred. No. 2.2e-29;
65; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354 LGVALDD-ERİKYASKAGKENIPLDWALGAFILN 386
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31.2%;
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A;Cross-references: SGD:S0000807
A;Map position: 5R
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C. Accession: G8442

R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, M.J.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, L.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID: 20083487; PMID: 10617197

A;Status: preliminary
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        418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 GALDLGGASTQVTF-VPQNQTIESPD------NALQFRLYGKDYNVYTHSFLCYGK 258
                                                                                                                                                                                                                                              169 GFLDMGGASVÓIAFELPPSOLKNYKDSISTVHIGLQNGQOL----EYPLFVTTWLGFGA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321 DVFDMGGSYHFPNFYKKVDE----YCGTEWETMLSRLYNKELTPSTDENKLEKLCFKASW 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----YHFTADSWEHIHFIGKIQGSDAGWTLGYML 456
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                                                                                                                                                                                                                                                                                                                                                                                                       316 IQGIGNYQQCHQSILELFNTSY-CPYSQCAFNGIFLPPLQGDFGAFSAFYFVMKFLNLTS 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable nucleoside triphosphatase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                  259 DQALWQKLAKDIQVASNEI----LRDPCFHPGYKKVVNVSDLYKTPCTKRFEMTLPFQQFE
                                                                                                                                                                                                                                                                                                                                   264 FAGTGDLKQCLKLTYNLLNKDKPCSMDPCNFDGISIPPV--DF-ANTEFVGVSEFWYTTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 EKVSQ-----EKVTEMMKKFCAQPWEEI-----KTSYAGVKEKYLSEYCFSGTY
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                                                                                       SL-SNYPFDF----QGARIITGQEEGAYGWITINYLLGKFSQKTRWFSIVPYETNNQETF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 YLGATAGMRLLRMESEBLADRVLDVVERSL--SNYPFDFQGARIITGQEBGAYGWITINY
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26.5%; Pred. No. 2.2e-25;
ive 81; Mismatches 236; Indels
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C;Superfamily: nucleoside triphosphatase chromatin-associated
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Matches 136; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-516 <STO>
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                                   64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable nucleotide phosphatase - fission yeast (Schizosaccharomyces pombe)
Cispecies: Schizosaccharomyces pombe
Cispecies: Schizosaccharomyces pombe
Cispecies: On-bec-1999 #sequence_revision 03-bec-1999 #text_change 09-Jul-2004
Ciscession: T40856
R;Ramsperger, U.; Pohl, T.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
A;Reference number: Z21952
A;Reference number: Z21952
A;Accession: T40856
A;Statuse: preliminary; translated from GB/EMBL/DDBJ
A;Residues: DNA
A;Residues: 1-572 <RAM>A;Residues: 1-572 <RAM
A;Residues: 1-572 <RA
                                                            25;
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DHFTFGFMDMGGASTQIAFAPHDSGEIARHRDDIATIFLKSVNGDLQ-----KWDVFVS 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        408 YLSEYCFSGTYILSLILQGY---HFTADSWEHIH-----FIGKIQGSDAGWTLGYML-- 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : |: |: |: | : | : | 450 ASGSILAGNDDFMYGIAPSERRTKLTGKKFIPGKLLESDQLRKQSSSLSNKGFLMWFAII 509
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                                                                                                                                        SKFVQKVNE-IGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELADRVLD
                                                                                                                                                                                                                                              SFEKKPQDAYKSHIKPLLDFAKNIIPESHWSSCPVFIQATAGWRLL---PQDIQSSILD
                                                                                                                                                                                                                                                                                                                  151 VVERSLSNYPFDF-----QGARIITGQEEGAYGWITINYLLGKFSQKTRWFSIVPYETN
                                                                                                                                                                                                                                                                                                                                                                                                                          205 NQETFGALDLGGASTQVTFVPQNQ------TIESPDNALQFRLYGKDYNVYTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFLCYGKDQALWQKLAKDIQVA-----SNEILRDPCFHPGYKKVVNVSDLYKT
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        Length 630;
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16.9%; Score 455.5; DB 2;
llarity 25.0%; Pred. No. 5.4e-28;
Conservative 103; Mismatches 170;
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                        al Similarity
139; Conserv
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Query Match
Best Local S
Matches 139
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Cyactesion: C86276
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chacesion: C86276
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chi, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Johnkin, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Rizzo, M.; Rooney, T.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MuID:21016719; PMID:11130712
A;Accession: C86276
A;Status: preliminary
A;Accession: C86276
A;Residues: 1-508 <STO>
A;Cross-references: UNIPROT:09XI63; GB:AE005172; NID:g5080800; PIDN:AAD39310.1; GSPDB:GN(C) Cydnetics:
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                                                      493
                                                                                                         458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 LPGFLADKGKFTATL-----QAAGNFSECRSAAFAMLQEEKGKCTYKRCSIGSIFTPN 345
345 KYCQKDWNDIQDGFKRNEFPNADIERLGTNCFKAAWVTSVLHDG--FNVDKTKHLFQSVL 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 KENDIGVVHQVEECRVK-GPGISKFVQKVNEIGIYLIDCMERAREVIPRSQHQETPVYLG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296 LYKTPCTK-RFEMTLPFQQFELQGIGNYQQCHQSILELF--NTSYCPYSQCAFNGIFLPP 352
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                                                                                                                                                                                                                                               7A19.33 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346 LQGSFLATENFFHTSKFFGL-GEK---EMLSEMILAGKRFCGEEWSKLKVKXPTFKDENL
                                                                                  || | : | || || : | || || 403 KIAGEEMQWALGAMLYHSKDLKFNLLEQLEVAQ--STQQISNFFSFFVIL--IIVLAVAL
                                                      442 KIOGSDAGWTLGYML-----NITNMIPAEQPLSTPLSHSTYVFLMVLFSLVLFTVAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 SKNILAILGFSSIIAVIALLAVG---LTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 TKSIIFVI-VACVTIALGLLFIGYSILRSGRNRRVSLHYSVIIDGGSSGTRVHVFGYRIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 ATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 SOKTRWFSIVPYETNN-OETFGALDLG-----GASTQVTFVPQNQTIESPDNALQFRLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 GK-DYNVYTHSFLCYGKDQALWQKLAKDI-QVASNE----ILRDPCFHPGYKKVVNV-SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||| ||:||:|| LRYCFSSAYIISMLHDSLGVALDD-ERIKYASKAGEEDIPLDWALGAFILN 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 410 SEYCESGTYILSLILQGYHFTADSWEHIHFIGKIQGSD--AGWTLG-YMLN 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 508;
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C;Superfamily: nucleoside triphosphatase chromatin-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.9%; Score 402.5; DB 2; 27.4%; Pred. No. 6.4e-24; ive 81; Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 27.44
Matches 129; Conservative
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hypothetical protein R07E4.4 - Caenorhabditis elegans

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uncleoside triphosphatase precursor, chromatin-associated - garden pea CiSpecies: Pisum sativum (garden pea) CiState: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004 CiStacession: 865147; 848859 CiStation  865141; MUID:96197404; PMID:8616230 Apacession: 865147 Apacession
                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    278
                                                                                                                                                                                                                                                                                                                                                                                                                        KDGVSILEGSMEGIYAWITINYLLGTLGGKA-----THSTVAVMDLGGASTQLV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |-----KALYKDKNCPVRPCSFNGVHQPKFTETFTDSPIYLISYFYDRMISLGMPS- 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294 FEPRFASDGESLVDGDHKYVLDYNGEQYELYQHSHLGYGLKEA--RKLIHKFVLNNAEAL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RD-----TLPFQQFEIQGIG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       352 KESLELLGDSTSIIHPCLH-----LNASLTHPDSKSEASEVVFVGPSLAHLSLQCRGIA 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 NYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFG----AFSAFYFVMKFLNLTSE 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376 KVSQEKVTEMMKKFCAQP--WEEIKTSYAGVXE-KYLSEYCFSGTYILSLLLQGYHFTAD 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 ISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELADRVLD 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 VVERSLSN-YPFDFQ--GARIITGQEEGAYGWITINYLLGKFSQKTRWFSIVPYETNNQE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84
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                                                                                                                                                                                                                                                               48 KYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEE--CRVKGPGISKFVQKVNEIGIYL
                                                                                                                                                                                                                                                                                                  106 TDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSN-YPFDF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FVPQ----NQTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -QGARIITGQEEGAYGWITINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 LTQNKAL---PENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVH----QVEECRVKGPG
                                                                                                                                                                                                     Gapa
                                                                                                                                                                                                  73;
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                                                                                                                                         556;
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                                                                                                                                                                                                  Indela
                                                                                                                                            Length
                                                                                                                                      Query Match 14.1%; Score 381.5; DB 2; Best Local Similarity 27.1%; Pred. No. 3.4e-22; Matches 121; Conservative 71; Mismatches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWEHIHFIGKIQGSDAGWTLGYMLNL 458
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                                            A;Gene: SPDB:SPAC824.08
A;Map position: 1
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C; Species: Caenorhabditis elegans
C; Date: 20-Sep-1999 #text_change 20-Sep-1999
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C; Accession: T16696
A; Description: The sequence of C. elegans cosmid R07E4.
A; Reference number: 218561
A; Reference number: 218561
A; Rocession: T16696
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Rolecule type: DNA
A; Rolecule type: DNA
A; Rolecule style: 1-557 *MLL>
A; Cross-references: EMBL: U39562; NID: 91049390; PID: 91049394; PIDN: AAA80403.1; CESP:R07E4
A; Experimental source: strain Bristol N2
C; Genetics:
C; Genetics:
C; Genetics:
A; Introns: 39/1; 67/1; 145/2; 192/1; 244/3; 317/3; 451/3; 488/2
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C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change O9-Jul-2004
C;Accession: T39109
R;Barrell, B.G.; Rajandream, M.A.; Quail, M.; Seegar, K.; Harris, D.
submitted to the EMBL Data Library, October 1999
A;Reference number: Z21828
A;Accession: T39109
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-556 cBAR>
A;Residues: 1-556 cBAR>
A;Experimental source: strain 972h-; cosmid c824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 D----TGVVHQVEECRVK-GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATAGMRLLRMESEELADRVLDVVERSLSN-----YPFDFQGARIITGQEEGAYGWIT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INYLLGKFSQ-KTRWFSIVPYETNNQETFGALDLGGASTQVTF-VPQNQTIES----- 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 LGCREDDSL-FK----YKLFVITFLGYGVNEGIRKYEHMLLSKLKDQNGTVIQDDCMPL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYKKVVNVSDLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFN----TSYC--P 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 NLHKTVTLEN------GENFVRRGTGNWNTCSNEVKKLINPESSSEVCKAE 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340 YSQCAFNGIFLP--PLQG-DFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEE 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346 AAKCYFGAVPAPSIPLSNIEMYGFSEYWYSTHDVLGLGGQYDAENIAKKTQQYCSKRWST 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         397 I----KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHF--IGKIQGSDAG 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               406 IQAESKKOLYPRADEERLRTQCFKSAWITSVLHDG--FSVDK-THNKFQSVSTIAGQEVQ 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 ELIQIEPVIYDNKPVMKKISPGLSTFGTKPAQAAEYLRPLMELAERHIPEEKRPYTPVFI
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14.7%; Score 397; DB 2; Lv
Best Local Similarity 25.0%; Pred. No. 2e-23;
Matches 133; Conservative 96; Mismatches 218;
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Qy 489 FTVALIGLE 498 	RESULT 13 JC4616 apyrase (EC 3.6.1.5) precursor - potato N;Alternate names: adenylpyrophosphatase; ATP-diphosphohydrolase C;Species: Solanum tuberosum (potato) C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004 C;Accession: JC4616; PC4147	R, Handa, M.; Guidotti, G. Biochem Biochem Roppya. Res. Commun. 218, 916-923, 1996 A;Title: Purification and cloning of a soluble ATP-diphosphohydrolase (Apyrase) from pote A;Reference number: JC4616; MUID:96158985; PMID:8579614	A;Accession: UC4016 A;Molecule type: mRNA A;Residues: 1-454 <han> A;Cross-references: UNIPROT:P80595; GB:U58597; NID:g1381632; PIDN:AAB02720.1; PID:g13816: A;Accession: PC4147</han>	A, Molecule type: protein A, Molecule 1995; 96-131;132-160;236-253;332-345 cHA2> A, Residues: 59-95; 96-131;132-160;236-253;332-345 cHA2> A, Residues: 59-95; 96-131;132-160;236-253;332-345 cHA2> A, Rote: The authors translated the codon GCA for residue 215 as Gly C; Comment: This enzyme belongs to a family of E-type ATPases, and it catalyzes the hydroll enzyme has nucleotide substrate specificity, divalent cation requirement, and insensiting olved in starch synthesis. C; Genetics: A; Genetics:	C;Keywords: glycoprotein; hydrolase; transmembrane protein C;Keywords: glycoprotein; hydrolase; transmembrane protein F;1-30/Domain: signal sequence #status predicted <sig> F;8-25/Domain: transmembrane #status predicted <tmm> F;31-454/Product: ATP-diphosphohydrolase #status predicted <mat> F;44-65/Region: actin-heat shock protein 70-hexokinase beta-phosphate binding F;192-212/Region: nucleotide binding #status predicted F;192-212/Region: actin-heat shock protein 70-hexokinase gamma-phosphate binding F;192-212/Region: nucleotide binding #status predicted F;30-410, 427-446/Region: hydrophobic carboxyl end F;30-410, 427-446/Region: hydrophobic carboxyl end</mat></tmm></sig>	Query Match  Query Match  Query Match  Query Match  Matches 118; Conservative 85; Mismatches 193; Indels 83; Gaps 19;		75	Qy 135 RLLRMESEBLADRVLDVVERSLSNYPFDFQGARIITGQEBGAYGWITINYLLGKFSQ 191  : :::  ::   ::	Qy 192 KTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQN-QTIESPDNALQFRLYGK 244 :	Qy 245 DYNVYTHSFLCYGKDQALWQKLAKDIQVASNBILRDPCPHPGYKKVVNVSDLYKTPCTKR 304	Qy 305 FEWTLPFQQFEIQGIGNYQQCHQSILELFN-TSYCPYSQCAFNGIFLPPLQGDFG 358	359AFSAPYFVMKFLNLTSEKVSQBKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSE	555 THASSERTUIGAÇÕIVULKESALARIGIUNARVAÇÕINVALIKSIERI
Qy 208 TFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYTHSFLCYGKD 259	QY         260 QALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTPCTKRFEMTLPFQQ 313           :               :             :   :           :   :   :           :   :   :           :   :   :   :           :   :   :   :   :           :   :   :   :   :           :   :   :   :           :   :   :   :   :           :   :   :   :   :           :   :   :   :   :   :           :   :   :   :   :   :   :   :   :   :	QY 366 VMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEY-CFSGTYI 419 bb 341 LPEDTGWVDASTPNFILRPVDIETKAKEACALNFEDAKSTYPFLDKKNVASYVCMDLIYQ 400	Qy 420 LSLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIP 463 	RESULT 12 T04439 hypothetical protein T18B16.150 - Arabidopsis thaliana hypothetical protein T18B16.150 - Arabidopsis thaliana ("C.Speciese: Arabidopsis thaliana (mouse-ear cress) C.Speciese: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004 C.Accession: T04439 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004 C.Accession: T04439 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004 B.Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Bancroft, I.; Mewes, H.Washinted to the Protein Sequence Database, April 1998 A;Reference number: Z15359	A.Accession: T04439 A.Molecule type: DNA A.Molecule type: DNA A.Residues: 1-1052 <bev> A.Cross-references: UNIPROT:049676; EMBL:AL021687 A.Experimental source: cultivar Columbia; BAC clone T18B16 A.Experimental source: cultivar Solumbia; BAC sone T18B16 A.Map position: 4 A.Introns: 79/3; 118/3; 217/1; 295/3; 396/3; 531/2; 815/3 A.Note: T18B16.150</bev>	Query Match 13.0%; Score 352; DB 2; Length 1052; Best Local Similarity 26.5%; Pred. No. 1.9e-19; Matches 114; Conservative 81; Mismatches 165; Indels 70; Gaps 18;	Qy 89 PGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR-MESEELADR 147	148 VLDVVERSLSNYPPDFQGARIITGQEEGAYGWITINYLIGKFSQKTRWFSIVPYE	203 TNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQA- 	Qy 262LWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTPCTKRFEMTLPFQ 312	Qy 313QFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGAFSAFYFVMKF 369  193 SGVSIKLVGAPNWGECSALAKNAPCALPDGY-PRPHGQFYAVSGFFVVYRF 842	QY 370 LNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHF 429	Qy 430 TADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFL-MVLFSLVL 488	

C.B.,

PID:9349

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A;Cross-references: EMBL:U18779; NID:g603625; PIDN:AAB65000.1; PID:g603637; MIPS:YEL042° C;Genetics: A;Gene: SGD:GDA1
                                                                                                                                   sphingolipid glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.; Wei, Y.; Taylor,
                                                                                                                                                                                                                    A, Molecule type: DNA
A, Residues: 1-518 cABES
A, October type: DNA
A, Residues: 1-518 cABES
A, October type: DNA
A, Cossion: B4073
A, Mote: sequence extracted from NCB1 backbone (NCBIN:134708, NCBIP:134711)
A, Accession: B4073
A, Mote: sequence extracted from NCB1 backbone (NCBIN:134708, NCBIP:134711)
A, Molecule type: protection
A, Residues: 125-144;238-257;276-281;366-174;399-412 cAB2>
R; Mulligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor
B, Mulligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor
B, Molecule type: DNA
A, M
                                                                      K.; Hirschberg,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----QGDFGA 359
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C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004 (C;Accession: A40732; B30837; S50502 (C;Accession: A40732; B40732; S30837; S50502 (S;Abeljon, C.; Yanaqisawa, K.; Mandon, E.C.; Hausler, A.; Moremen, K.; Hirsc J. Cell Biol. 122, 307-323, 1993 (A;Tille: Gamonaine diphosphatase is required for protein and sphingolipid gl A;Reference number: A40732; MUID:93308137; PMID:8391537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVGLTQNKALPENVKYGI VLDAGSSHTSLY I YKWPAEKENDTGVVHQVEECRVKGPGI SK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: nucleoside triphosphatase chromatin-associated
C;Keywords: glycoprotein; Golgi apparatus; hydrolase; transmembrane proteir
F:10-24/Domain: transmembrane #status predicted <TMM>
F:10-23/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae cosmids 8199, 8334, and
A;Reference number: S50491
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A;Molecule type: DNA
A;Residues: 1-518 <DIE>
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C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL: Z83113; PIDN: CAB05544.1; GSPDB: GN00023; CESP: KQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 KENDIGUVHQVEE---CRVKGPGISKFVQKVNEIGIYLIDCMERAREVIPRSQHQETPVY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : |: :||: :||: ASH--GMPFKVEKEIFQEVK-PGLSSFAKSPSSAADSLEPLLQRARKEVPHFWEKTPIT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGATAGMRLLRMESEELADRVLDVVERSLSNYPF--DFQGA-RIITGQEEGAYGWITINY 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333 PVYLFSYFFDRALNSGLVKGNEGGKIELRQFKEAAEIACRREKTEIDDG-----SHWMPW 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
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                                                                      LCMDLIYEYTLLVDG--FGLNPHKEITVIHDVQYKNYLVGAAWPLGCAIDLVSSTTNKI 449
                                                                                                                                                                                                                                                   hypothetical protein KO8H10.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 LAILGFSSIIAVIALLAVGLTQNKALPENVK----YGIVLDAGSSHTSLYIYKW---PAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 ILLISFESLLSVVTTKTQYWCHGDGVLNNQHTCRFFTIVIDAGSTGTRLHLYKFIHDPAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 --FGHHIRLFTHSFLGNGLIAARLNILQLETDNEIESTHQLITSCMPEGYQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLGK-FSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESP----DNALQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 LLETLFTDE----PTVGHKPAAHRSVAAFDLGGGSTOLTYWPNNEAVFSEHVGYERDIDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIP-AEQPLST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72;
                                                                                                                                                                                                                                                                              C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 05
C; Accession: T23508
R; Gardner, A.
submitted to the EMBL Data Library, November 1996
A; Reference number: 219750
A; Reference number: 219750
A; Reference number: 219750
A; Residues: 1-479 *MIL.
A; Experimental source: clone K08H10
C; Genetics:
A; Gene: CESP: K08H10.4
A; Map position: 5
A; Introns: 36/3; 83/3; 189/1; 300/2; 412/3
C; Superfamily: nucleoside triphosphatase chromatin-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.3%; Score 332; DB 2; Length 47 26.1%; Pred. No. 2.3e-18; ive 80; Mismatches 211; Indels
                                 YCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSD-
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A40732
guanosine-diphosphatase (EC 3.6.1.42)
N/Alternate names: protein YEL042w
C;Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 26.19
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLS---HSTYV 478
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465 LSPQVSLLHTGYDIPLQ--RELRIGKKIANKEIGWCLGASLPL 505

Search completed: September 21, 2005, 16:21:57 Job time : 29 secs

schistosoma

torpedo mar arabidopsis arabidopsis arabidopsis arabidopsis oryza sativ mus musculu candida gla arabidopsis brachydanio arabidopsis arabidopsis

07yta4 08k012 08x162 09x162 094ap8 08b1d8 08ccv2 06frc2 06drc2 06drc2

Q7YTA4 Q8K0L2 Q8K0L2 Q8K1K2 Q8K1K2 Q6K1G8 Q8H1D8 Q8H1D8 Q8CCV2 Q6FRC2 Q9FEC2 Q9FEC2 Q6GH30 Q6GFRC2

223.9 223.3 223.3 118.5 118.5 117.0 117.0 117.8 117.8 117.8

6698.5 5596.5 5111.5 5111.5 5101.5 510.5 549.5 69.5 69.5

ALIGNMENTS

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September 21, 2005, 13:13:33 ; Search time 91 Seconds (without alignments) 2869.894 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Title: Perfect score: Sequence: Scoring table: Searched:	US-09-807-660C-2 2698 I MEDTKESNVKTFCSKNILAIVAIIGLLIFHKPSYFWKDMV 510 BLOSUM62 Gapop 10.0 , Gapext 0.5 1612378 segs, 512079187 residues
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2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	P49961 homo sapien	P55772 mus musculu	BUM	Q8cdv7 mus musculu	P97687 rattus norv	Q9myu4 sus scrofa	Q86vv3 homo sapien	O18956 bos taurus	Q8cebl mus musculu	Q6dfsl xenopus tro	Q6gp74 xenopus lae	Q6dc46 brachydanio		gallus	gallus	035795 rattus norv	O55026 mus musculu	Q921r1 mus musculu		P79784 gallus gall		Q66164 brachydanio	Q7t014 brachydanio	Q6nvi9 xenopus tro	O75355 homo sapien	Q6uvz0 homo sapien	Q9y513 homo gapien	6 rattu	Q8bfw6 m mus muscu	Q6zm68 brachydanio	Q8n6k2 homo sapien
ID	ENP1 HUMAN	ENP1 MOUSE	<u>0921</u> <u>0</u> 6	Q8CDV7	ENP1 RAT	ENP1_PIG	Q86V <u>V</u> 3	ENP1 BOVIN	Q8CEB1	Q6DFS1	Q6GP74	Q6DC46	Q6UQ22	ENP1_CHICK	090x66	ENP2_RAT	ENP2_MOUSE	Q921R1	Q62M69	ENP2_CHICK	Q6GNA4	Q66L64	Q7T014	Q6NVI9	ENP3 HUMAN	06UVZ0	ENP2 HUMAN	Q802 <u>2</u> 6	QBBFW6	Q6ZM68	Q8N6K2
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Query Match	100.0	77.7	77.5	77.0	76.3	•	٠			57.5		50.9		38.2		37.2	37.1	37.1	36.4	36.4	36.4	36.1	•	٠	34.9	34.8	34.8	34.7	•	31.9	31.3
Score	2698	2096	2091	2077	2057.5	2006	1993	1982.5	1693	1552	1530	1373.5	1063.5	1029.5	1014.5	1004	1001	1001	982	981.5	981	975	973.5	950	942.5	940	939.5	937.5	$\sim$	860.5	843.5
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Name=Placental II;

Name=Placental II;

Isoid=P49961-3; Sequence=VSP_003607, VSP_003608, VSP_003609;

TISSUE SPECIFICITY: Expressed primarily on activated lymphoid or and specific primarily on activated lymphoid on a specific primarily on activated specific primarily on activated lymphoid on the placental isoform II are present in both placenta and the placental isoform II are present in placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Koziak K., Kaczmarek E., Kittel A., Sevigny J., Blusztajn J.K.,
Schulte Am Esch J. II, Imai M., Guckelberger O., Goepfert C., Qawi I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleotics to regulate purinergic neurotransmission. Could also be implicated in the prevention of platelet aggregation. Could also Hydrolyzes ATP and ADP equally well.

CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
COPACTOR: Requires calcium and magnesium.
SUBUNIT: Homodimer; disulfide-linked (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                     Makita K., Shimoyama T., Sakurai Y., Yagi H., Matsumoto M., Narita N Sakamoto Y., Saito S., Ikeda Y., Suzuki M., Titani K., Fujimura Y.; "Placental ecto-APP diphosphohydrolase: its structural feature distinct from CD39, localization and inhibition on shear-induced Int. J. Hematol. 68:297-310(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Palmitoylation targets CD39/endothelial ATP diphosphohydrolase to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: The N-terminus is blocked.
MISCELLANEOUS: Optimal pH is 7.0-7.5 with ATP as substrate and 7.5-8.0 with ADP.
                                                                                                                                                                                                                               MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116; Kaczmarek E.; Koziak K.; Sevigny J.; Siegel J.B., Anrather J.; Beaudoin A.R., Bach F.H., Robson S.C.; "Identification and characterization of CD39/vascular ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96215267; PubMed=8626624; DOI=10.1074/jbc.271.17.10391; Wang T.F., Guidotti G.; "CD39 is an ecto-(CG2+,Mg2+)-apyrase."; J. Biol. Chem. 271:9898-9901(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PALMITOYLATION.
MEDLINE=20102721; PubMed=10636909; DOI=10.1074/jbc.275.3.2057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 275:2057-2062(2000). - FUNCTION: In the nervous system, could hydrolyze ATP and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the GDA1 / CD39 NTPase family. DATABASE: NAME=PROW; NOTE=CD guide CD39 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd39.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P4996i-1; Sequence=Displayed;
Name=Placental 1;
                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 271:33116-33122(1996)
  MEDLINE=99062444; PubMed=9846014;
                                                                                                                                                                                                                                                                                                                                      diphosphohydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Vascular;
                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Robson S.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  caveolae.";
J. Biol. Ch
-!- FUNCTIO
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                                                                                                                                                                                                       Cytoplasmic (Potential).
N-linked (GlCNAc. .) (Potential).
I and isoform Placental II).
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PFTSAPPAPTSCCFLFQIQ (in isoform Placental
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GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0007596; P:blood coagulation; TAS.
InterPro; IPR004040; GDA1_CD39_NTPase.
Pfan; PF01150; GDA1_CD39_1.
PROSTIE; PS01238; GDA1_CD39_NTPASE; 1.
Alternative splicing; Antigen; Calcium; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId=VSP_003608.
Missing (in isoform Placental II).
/FTId=VSP_003609.
SF 1-2 Gin Ref. 5).
D -> K (in Ref. 4).
T -> TGET (in Ref. 5).
V -> Y (in Ref. 5).
W -> Y (in Ref. 5).
W -> Y (in Ref. 5).
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                                                                                                         Glycoprotein; Hydrolase; Lipoprotein; Magnesium; Palmitate;
                                                                                                                                                                                                                                                                                                                                                                                     VASNEILRDPCFHPGYKKVVNVSDLYKT
                                                                                                                                                           Potential.
Extracellular (Potential).
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510 AA;
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EMBL, S73813; AAB32152.1; -. EMBL, U87967; AAB47572.1; -. BERL; AJ133133; CAB41886.1; -. EMBL, AJ133134; CAB41887.1; -.

PIR; 156242; 156242. Genew; HGNC:3363; ENTPD1. MIM; 601752; -.

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CARBOHYD
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-!- FUNCTION: In the nervous system, could hydrolyze ATP and other nucleotides to regulate purinergic neurotransmission. Could also be implicated in the prevention of platelet aggregation. Hydrolyzes ATP and ADP equally well.

-!- CATALYTIC ACTIVITY: ATP + 2 H(2)0 = AMP + 2 phosphate.
-!- COPACTOR: Requires calcium and magnesium (By similarity).
-!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE_55015846; PubMed=7930580; Maliszewski C.R., Delespesse G.J.T., Schoenborn M.A., Armitage R.J. Fanslow W.C., Nakajima T., Baker E., Sutherland G.K., Poindexter K. Birks C., Alpert A., Friend D., Gimpel S.D., Gayle R.B. III; "The CD39 lymphoid cell activation antigen. Molecular cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Frank, Fr
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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GO; GO:0006200; P:ATP catabolism; IDA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
GO; GO:0030168; P:platelet activation; IDA.
GO; GO:000311; P:purine ribonucleoside diphosphate catabolism;
InterPro; IPR000407; GDAL_CD39_NTPase.
PF01150; GDAL_CD39; I.
                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Last Sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
(NTPDasel) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid activation antigen) (Ecto-apyrase) (CD39 antigen).
Mame-Entpdl; Synonyms-Cd39;
Mus musculus (Mouse).
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MEDLINE=9839871; PubMed=9730622;
Schoenborn M.A., Jenkins N.A., Copeland N.G., Gilbert D.J.,
Schoenborn Maliazewski C.R.;
"Gayle R.B. III, Maliazewski C.R.;
"Gene structure and chromosome location of mouse Cd39 coding
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MEL, AF041812, AAC83203.1;

MEL, AF041812, AAC83203.1;

JOINED.

MEL, AF041814, AAC83203.1;

JOINED.

MEL, AF041815, AAC83203.1;

JOINED.

MEL, AF041815, AAC83203.1;

JOINED.

MEL, AF041817, AAC83203.1;

MEL, AAC83203.1;
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                                                                                                                                                                                           (Rel. 35, Created)
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SEQUENCE FROM N.A.
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P55772;
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                                              Cycoplasmic (Potential).
N-linked (GlCNAc. .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                           4.
                                                                                                                                                                                                    Length 510;
                                                                                                                                                                                                                                        66; Indels
                   Extracellular (Potential).
                                                                                                                                                                       8E6A6113D2E13930 CRC64;
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Last annotation update)
                                                                                                                                                                                                      Score 2096; DB 1;
Pred. No. 5.4e-150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 5.4e
53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
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                                   Potential
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                                                                                                                                                                       57205
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Name=Entpdl;
TRANSMEM
DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
CARBOHYD
                                                                                                                                  CARBOHYD
CARBOHYD
SEQUENCE
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F., Statchenko L., Marueina K., Farmer A.A., Rubin G.M., Hong L., Statchenko L., Marueina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Carainci P., Frange C., Brownstein M.J., Usdin T.B., Tochiyuki S. Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Pilahon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., Jones S.J., Marra M.A., Jones S.J., Marra M.A., St., T. Generation and initial analysis of more than 15,000 full-length human an ouse CDNA sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGAF 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAFYFVMKFLNLTSEK--VSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTY 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L; BC011278; AAH11278.1; -...
; MGI:102805; Entpdl.
GO:0005605; C:basal lamina; IDA.
GO:0016021; C:integral to membrane; TAS.
GO:0016020; P:apyrase activity; IDA.
GO:000180; P:apyrase activity; IDA.
GO:000180; P:ATP catabolism; IDA.
GO:000180; P:platelet activation; IDA.
GO:000181; P:platelet activation; IDA.
GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.
m; PF01150; GDA1_CD39; 1.
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Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011278; AAAH11278.1; -.
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[3]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research "Analysis of the mouse transcriptome based on functional annotation of "Analysis of the mouse transcriptome based on functional annotation of "Analysis of the mouse transcriptome based on functional annotation of "Analysis";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Testis; MEDLINB=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Fromo H., Okazaki Y., Muramatsu M., Hayashizaki Y., Fromo H., Okazaki Y., Muramatsu M., Hayashizaki Y., Fromo Historian ond Subtraction of Cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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STRAIN=C57BL/6J; TISSUB=Testis;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Hanawa T., Hara A., Hashizume W., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-CSTBL/60; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
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STRAIN=C57BL/6J; TISSUE=Testis;

MEDLINE=2539013; PubMed=11076861; DOI=10.1101/gr.152600;

MEDLINE=2539013; PubMed=11076861;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamanoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yoneda Y., Ishikawa T., Ogawa Y., Izawa M., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Ilnoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male testis cDNA, RIKBN full-length enriched
library, clone:4921311005 product:ectonucleoside triphosphate
diphosphohydrolase 1, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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479 GLMVLFSLLLVAVAITGLFIYSKPSYFWKEAV
                                                                                                                                                          Created)
                                                                                                                                                          (TrEMBLrel. 23,
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                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                    (Mouse).
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                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                              Name=Entpd1;
                                                                                                                                                            01-MAR-2003
                                                                                                               Q8CDV7
                                                                RESULT
Q8CDV7
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Chordata; Craniata; Vertebrata; Euteleostomi;

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Eukaryota; Metazoa;
       Salto R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
A Tagawa A., Toya U., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
BMB1: AK029512; BAC26486.1; --
RMG1:102805; Entpdl.
RMG1:102805; Entpdl.
RMG2; GO:0005605; C:basal lamina; IDA.
GO: GO:0005605; C:basal lamina; IDA.
GO: GO:0005605; C:basal lamina; IDA.
RMG0; GO:0007186; P:ATP catabolism; IDA.
GO: GO:000181; P:Purine ribonucleoside diphosphate catabolism; IDA.
RMG0; GO:000181; P:purine ribonucleoside diphosphate catabolism; IDA.
RMG0; GO:0000181; C:D39_NTPase.
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                                                                                                                                                                                                                                                                                                                                                                                   PVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINY 184
                                                                                                                                                                                                                                                                                                                                                                                                                                   LLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGK 244
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                                                                                                                                                                                                                                                                                                                                                     94 YKWPAEKENDTGVVQQLEECQVKGPGISKYAQKTDEIGAYLAECMELSTELIPISKHHQT
                                                                                                                                                                                                                                                                                                                                                                                                154 PVYLGATAGMRLLRMESEQSADEVLAAVSTSLKSYPFDFQGAKIITGQEEGAYGWITINY
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16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
(NTPDasel) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cactivation antigen) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cactivation antigen) (Ecto-apyrase) (CD39 antigen).
                                                                                                                                                                                                                                           Length 539;
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                                                                                                                                                                                                                                          77.0%; Score 2077; 75.8%; Pred. No. 1.
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                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-Wistar; TISSUE-Cochlea;
MEDLINE-20050856; Pubmed=10581401; DOI=10.1016/S0169-328X(99)00244-2;
Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Sprague-Dawley; TISSUE=Brain;
MEDLINE=99031057; Pubbed=9364474; DOI=10.1016/S0028-3908(97)00115-9;
KGGPL B., Braun N., Heine P., Maliazewaki C.R., Zimmermann H.;
"An ecto-ATPase and an ecto-ATP diphosphohydrolase are expressed in
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                                                                                                                                                         one ecto-
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Pfam; PF01150; GDA1_CD39; 1.
PR051TE; PS01238; GDA1_CD39 NTPASE; 1.
Antigen; Calcium; GDA1_CD30 Hydrolase; Magnesium; Transmembrane.
DOMAIN 1 16 Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                        Vlajkovic S.M., Housley G.D., Greenwood D., Thorne P.R.;
"Evidence for alternative splicing of ecto-ATPase associated with
termination of purinergic transmission.";
Brain Res. Mol. Brain Res. 73:85-92(1999).
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                                                                                                                              Aang T.-F., Rosenberg P.A., Guidotti G.; "Characterization of brain ecto-apyrase: evidence for only
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length
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Potential.

Cytoplasmic (Potential).

N-linked (GlCNAc. .) (Potential).
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                                                                                    STRAIN-Sprague-Dawley; TISSUE-Brain, and Hippocampus; PubMed=9221928;
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74.2%; Pred. No. 4.5e-147;
iive 58; Mismatches 71;
                                                                                                                                                                                                Res. Mol. Brain Res. 47:295-302(1997)
                                                                AND CHARACTERIZATION
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SEQUENCE OF 432-511 FROM N.A.
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Matches 380; Conservative
                                                                                                                                                                       gene.";
                                                                SEQUENCE FROM N.A.,
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                      NCBI_TaxID=10116;
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                      1 MEDIKOSKVKRPCSKNILLILGFSSSVLAVIALIAVGLTHNKPLPENVKYGIVLDAGSSHT
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MEDIJNE=97115868; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;
Racznarek E., Koziak K., Sevigny J., Siegel J.B., Anrather J.,
Racznarek E., Roziak K., Sevigny J., Siegel J.B., Anrather J.,
Beaudoin A.R., Bach F.H., Robson S.C.;
"Identification and characterization of CD39/vascular ATP
diphosphohydrolase.";
J. Biol. Chem. 271:33116-33122(1996).
J. Biol. Chem. 271:33116-33122(1996).
nucleotides to regulate purinergic neurotransmission. Could also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sevigny J.; "Distribution, cloning, and characterization of porcine nucleoside
                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2004 (Rel. 44, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
(NTPDasel) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell activation antigen) (Ecto-apyrase) (CD39 antigen).
Name-ENTPD1; Synonyms-CD39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20325090; PubMed=10866813; Lemmens R., Vanduffel L., Kittel A., Beaudoin A.R., Benrezzak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                      FLMVLFSLVLFTVAIIGLLIFHKPSYFWKDMV 510
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Eur. J. Biochem. 267:4106-4114(2000)
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TISSUE-Aortic endothelium;
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between the Swiss Institute of Bioinformatics and the EMBL outstation—
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 HQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MEDIKESNVKTFCSKNILAILGFSSIIAVIALLAVGLIQNKALPENVKYGIVLDAGSSHT
                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ133746; CAB95871.1; -.
InterPro; IPR00407; GDA1_CD39_NTPase.
Pfam, PF01150; GDA1_CD39; I.
PROSITE; PS01238; GDA1_CD39 NTPASE; 1.
Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subunit
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                                                                                                                                                                noncovalent interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diphosphohydrolase 1. Ectonucleoside triphosphate diphosphohydrolase 1 27 kDa Ectonucleoside triphosphate diphosphohydrolase 1 54 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ectonucleoside triphosphate
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Potential.
Extracellular (Potential).
Potential.
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82F86869040D7735 CRC64;
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(GlcNAc. . .)
(GlcNAc. . .)
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N-linked (GlCNAc. .)
N-linked (GlCNAc. .)
N-linked (GlCNAc. .)
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Matches 368; Conservative
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203
510 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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     61 VPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYTHSFLCYGK 120
                                                                               121 DQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTPCTKRFEMTLPFQQFEIQG
                                                                                                                                                                                      181 IGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVS
                                                                                                                                                                                                                                                                                                QEKVTEMMKKRCAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIH
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                                                                                                                                                        319 IGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVS
                                                                                                                                                                                                                                                                QEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIH
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                                                                                                                                                                                                                                                                                                                                                                                                  FIGKI QGSDAGWTLGYMLNLTNMI PAEQPLSTPLSHSTYVFLMVLFSLVLFTVAIIGLLI
                                                   DQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTPCTKRFEMTLPFQQFEIQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diphosphohydrolase.";
J. Biol. Chem. 271:33116-33122(1996).
-!- FUNCTION: In the nervous system, could hydrolyze ATP and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=ENTPD1; Synonyms=CD39;
Bos taurus (Bovine).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleotides to regulate puriners, course statements and could be implicated in the prevention of platelet aggregation. Could a Hydrolyzes ATP and ADP equally well.

-!- CATALYTIC ACTIVITY: ATP + 2 H(2)0 = AMP + 2 phosphate.
-!- COPACTOR: Requires calcium and magnesium.
-!- SUBURIT: Homodimer, disulfided-linked (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116; Kaczmarek E., Koziak K., Sevigny J., Siegel J.B., Anrather J., Beaudoin A.R., Bach F.H., Robson S.C.; "Identification and characterization of CD39/vascular ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ectorucleoside triphosphate diphosphotydrolase 1 (EC 3.6.1.5)
(NTPDasel) (Ecto-ATP diphosphotydrolase) (ATPDase)
activation antigen) (CD39 antigen) (Ecto-apyrase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 97-103; 123-133; 136-140; 145-168 AND 459-471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE-Actric endothelium;
Chang A.S., Garcia R.L., Chang S.M., Schilling W.P.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                513 AA.
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RA Atausner R.D., Collins F.S., Wagner L. Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bhar N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bhar N.K.,
RA Hopkins R.F., Jordan H., Moore T., Mang J., Hsieh F.,
Ra Biston M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Rapleton M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                              CTRRFLTSLPFPELEIQGTGDFQKCQQSIRPLFNTSYCPYSRCSFDGVFLPLPQGDFAAF 359
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                                                                                                                                                     LSLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVF
                                                                               SAFYFUMKFLNLTSEKVS-QEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC047664; AAH47664.1; -.
GO; GO:0016787; F:hydrolase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000407; GDA1_CD39_NTPase.
Pfam: PF01150; GDA1_CD39; 1.
PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
SEQUENCE 372 AA; 42731 MW; ABBIDE1366356EE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                             LMVLFSLVLFTVAIIGLLIFHKPSYFWKDMV 510
                                                                                                                                                                                                                                                                                        100.0%; Pred. No. 2.3
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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300
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                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
2086VV3
1D C086VV
AC Q86VV
DT O1-J
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DT O1-J
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musculus (Mouse).
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                      SEQUENCE FROM N.A.
                      NCBI_TaxID=10090;
 SLYIYRWPAEKENDTGVVTQIEESNVKGPCISGFAKKVNEINVYLTACMERAQKVIPSIQ 120
                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                                                                                    HQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWI 180
                                                                                                                                                                                                                                                                                                                                  LYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP 300
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                                                                                                                                                                                                                                                                                                                                                                                                GAFSAFYFVMKFLNLTSEK-VSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSG 416
                                                                                                                                                                                                                                                                                                                                                                                                          TYILSLLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHST 476
                                                                                                                                                                                                                                   SLYIYKWPAEKENDIGVVHQVEECRVKGPGISKFVQKVNEIGIYLIDCMERAREVIPRSQ 120
                                                                                                                                                                                                                                                                                                                                                                CTKRFEMT --- LPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDF 357
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                                                                                                                                                                                                                                                                                                             TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFR
                                                                                                                                                                                                              MEDIKESNVKTFCSKNILA1LGFSSI1AVIALLAVGLTQNKALPENVKYGIVLDAGSSHT
Pfam; PF01150; GDA1_CD39; 1.
PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 10 days menate skin cDNA, RIKEN full-length enriched
library, clone:4732419M16 product:ectonucleoside triphosphate
diphosphohydrolase 1, full insert sequence. (Fragment).
                                                              Cycoplasmic (Potential).
N-linked (GlcNAc. .) (Potential).
                                                                                                                                                                                     5
                                                                                                                                                                      DB 1; Length 513;
                                                                                                                                                                                     Indels
                                              Extracellular (Potential)
Potential.
                                                                                                                                                      20FE98F27B6D2F96 CRC64;
                                                                                                                             K -> N (in Ref. 2).
INV -> CGF (in Ref. 2).
K -> V (in Ref. 2).
                                 Cytoplasmic (Potential)
                                                                                                                                                                                     72;
                                                                                                                                                                             70.8%; Pred. No. 2.1e-141; ive 73; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YVFLMVLFSLVLFTVAIIGLLIFHKPSYFWKDMV 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.5%; Score 1982.5;
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                                                                                                                                                       58113 MW;
                                                                                                                                                                             Local Similarity 70.8
les 364; Conservative
                          Magnesium; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                 16
37
37
502
502
722
723
330
460
460
460
                                   Name=Entpd1
                                         TRANSMEM
DOMAIN
                                                                               CARBOHYD
CARBOHYD
CARBOHYD
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                                                                                                               CARBOHYD
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                                                        TRANSMEM
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                                                                       CARBOHYD
                                                                                                       CARBOHYD
                                                                                                                                                       SEQUENCE
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Matches
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De Mekryota, Metazoa, Chordata, Cranidara, Vertebreta, Buteleostomi, OX Mammalia, Eutheria, Eutheria, Stoincognathi, Muridae, Musina, OX Wammalia, Eutheria, Eutheria, Stoincognathi, Muridae, Musina, OX Wammalia, Eutheria, 1931-44(1999).

R. MEDLINES, ETRANDO, 1901-19-44(1999).

R. MEDLINES, EUTHERIA, EUTH
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SLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQKVNBIGIYLTDCMERAREVIPRSQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywalnski M.I., Skalaska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALLAVGLTQNKALPENVKYGIVLDAGSSHT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                  databases.
                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.5%; Score 1552; DB 2;
55.9%; Pred. No. 7.9e-109;
cive 92; Mismatches 131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similaricy ... hes 285; Conservative
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                                                                                                                                                                                                                                                                                                                        210
                                                                                                                                                                                                                                                                                                                                            61 AVSTSLKSYPFDFQGAKIITGQEEGAYGWITINYLLGRFTQEQSWLSLIS-DSQKQETFG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GWILGYMLNLTNMIPAEQPLSTPLSHSTYVPLMVLFSLVLFTVAIIGLLIFHKPSYFWKD 508
                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                          TISSUE-Embryo;
Straubsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Straubsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                      151 VVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKFSQKTRWFSIVPYETNNQETFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 ALDLGGASTQITFVPQNSTIESPENSLQFRLYGEDYTVYTHSFLCYGKDQALWQKLAKDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 QVASNEILRDPCFHPGYKKVVNVSDLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSIL
                                                                                                                                                                                                                                                                                                                                                                                                       ALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAKDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FCAQPWEEIKTSYAGVKEKYLSEXCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                    Length 420;
                                                                                                                                                                                          Indels
                                                                                 1
420 AA; 47261 MW; 1369E747CD4B9CE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                               62.8%; Score 1693; DB 2;
ilarity 73.9%; Pred. No. 1.3e-119;
Conservative 46; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          508 A.A.
InterPro; IPR000407; GDA1_CD39_NTPase.
Pfam; PF01150; GDA1_CD39; 1.
                                   PROSITE, PS01238, GDA1_CD39_NTPASE, 1.
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Name=entpdl-prov;
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                                                                                                                                                                   Similarity
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                                                                Hydrolase.
                                                                                    NON TER
SEQUENCE
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                                                                                                                                               Query Match
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                                                                                                                                                                      Best Loca
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1D 06DFS
AC 06DFS
AC 06DFS
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25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
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Matches 264; Conservative
                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                               Zgc:100819 protein.
Name=zgc:100819;
                                                                                                                                                                                                                                                                                                                                                                                Cyprinidae, Danio.
NCBI TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                    Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.P., Zeeberg B. A., Grouse L.H., Derge J.G.,

Altschul S.P., Zeeberg B. Buetow K.H., Schaefer C.F., Bahat N.K.,

Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

Antschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

An Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Sheychekv Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

" "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5,
                                                                 TISSUE=Spleen;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 508;
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klein S., Gerhard D.S.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BC071287; AAH73267.1; -0.60.60.0016787; F.Hydrolase activity; IEA. InterPro; IPR000407; GDAL_CD39_NTPase. Pfan; PF01150; GDAL_CD39_NTPASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57049 MW; BD205818A06C523B CRC64;
                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.7%; Score 1530; DB 2; 55.3%; Pred. No. 3.7e-107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                                            cDNA sequences.
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            Xenopodinae; Xenopus.
NCBL_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   508 AA;
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RX STRAIN-Singapore local strain; TISSUE-Embryo;

RX Straubberg RL, Feingold E.A., Grouse L.H., Derge J.G.,

Ry Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Straubberg R.L., Zeberg B., Bucrow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeberg B., Bucrow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Ry Vilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rapher J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Ry Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,

Ry Mones S.J., Marra M.A.;

Roberzation and initial analysis of more than 15,000 full-length human
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359 SAYYFVMDFLKLTKGEISLDKVKETVERHCSKPWDEVKKEFPKIKEKYLSEYCFSGTYIL 410
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                                                                                                      SAFYFUMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL
                                                                                                                                                                                                                                     SLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
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52.8%; Pred. No. 2.5e-95;
ive 82; Mismatches 131; Indels
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801238; GDA1_CD39 NTPASE; 1.
492 AA; 55507 МW; В789АВ6DFC6A032B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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STRAIN=Singapore local strain; TISSUE=Embryo;
Director MGC Project;
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                                                                                                                                                                                                                                                                                                                                                                       MYLFSLVLFTVAIIGLLIFHKPSYFWKDMV 510
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LQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFLMVL 483
                           |||:||:||| | : ||| | : ||| | HISYLCFGRDQILNRLIAKLAQDRLSSQVAP---VRHPCYHSGYQAILPLSSLYDSPCIHT
                                                                                                                                                                                                                                                                                                                                                     HSFLCYGKDQALWQKLAK-----DIQVASNEILRDPCFHPGYKKVVNVSDLYKTPCTKR
                                                                                                                                                                                                                                                                       298 IDSLNHTQNLTVEGTGDPGNCVVALRSLFNFSSCKGQKDCAFNGIYQPPVHGQFYAFSNF
                                                                                    QKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT
                                                                                                                                                                                                                                                305 FEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCP-YSQCAFNGIFLPPLQGDFGAFSAF
                                                                                                                                                                                                                                                                                                                                YFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLL
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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MEDLINE-97442428; PubMed=9295305; DOI=10.1074/jbc.272.38.23645;
MEDLINE-97442428: T.L.; Kirley T.L.;
Lumunolocalization of the ecto-ATPase and ecto-apyrase in chicken gizzard and stomach. Purification and N-terminal sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell
    MRLLRMESEELADRVLDVVERSLSNYPPDFQGARIITGQEEGAYGWITINYLLG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99298108, PubMed=9632655; DOI=10.1074/jbc.273.26.16043;
Nagy A.K., Knowles A.F., Nagami G.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
(MIPDasel) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid activation antigen) (Ecto-apyrase) (CD39 antigen)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nagy A.K., Knowles A.F., Nagami G.T.; "Molecular cloning of the chicken oviduct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSLVLFTVALIGLLIFHKPSYFW 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 273:16043-16049(1998)
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Gallus gallus (Chicken).
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                                                                                                                                                                                                                                                                                                                                                                                                                                LLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNWIPAEQPLSTPLSHSTYVFLM 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YNVYTHSFLCYGKDQALWQKLAKDIQVASNE----ILRDPCFHPGYKKVVNVSDLYKTPC 301
                                                                                                                                                                                                                                                                                                                           TKRFEMTLPFOOFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGAFS 361
                                                                                                                                                                                                                                                                                                                                                                                                         AFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYILS 421
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                       186 LGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKD
                                                                                                                                                                                287 MKPLKM--PKEQFSHVGLGNWSQCQESIRKVFNTSHCPYSGCSFNGVFQPTVEGKFGAFS
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                                                                             VYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYL
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Bigonnesse F., Levesque S.A., Kukulski F., Lecka J., Robson S.C., Fernandes M.J.G., Sevigny J.;
Fernandes M.J.G., Sevigny J.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AV364442; AAQ84519.1;
EMBL; AV364442; RAQ84519.1;
GO; GO:0004050; F.apyrase activity; IEA.
GO; GO:0016797; F.hydrolase activity; IEA.
InterPro; IPR004007; GDAl_CD39_NTPase.
Pfem; PF01150; GDAl_CD39; 1.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Nucleoside triphosphate diphosphohydrolase-8 (EC 3.6.1.5)
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PROSITE; PS01238; GDA1 CD39_NTPASE; 1.
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Mus musculus
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SEQUENCE
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Hydrolase.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MRILIRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLG---KFS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 DIGVVHQVEECRVKGPGISKFVQKVNBIGIYLTDCMERAREVIPRSQHQETPVYLGATAG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSFLCYGKDOA---LWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTPCTKRFEM 307
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                                                                                                           InterPro; IPR000407; GDA1_CD39_NTPase.
Pfam; PF01150; GDA1_CD39; 1.
PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
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N-linked (GlcNAc. .)
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54034 MW;
                                                                                                    EMBL; AF041355; AAC26491.1;
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493 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368 KFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 SFLNLTGQQ-SLSHVNATVWDFCNRNWSELVETFPQNKE-HLHTYCVVGLYILTLVDGY
                                                                                                                                                                                                                                                                                 Gallus gallūs (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 KNILAILGFSSIIAVIALLAVGL-TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKEN
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MEDLINE-21982040; PubMed=11985621;
MEDLINE-21982040; PubMed=11985621;
Knowles A.F., May A.K., Strobel R.S., Wu-Weis M.;
Purification, characterization, cloning, and expression of the chicken liver ecto-APT-diphosphohydrolase.";
EMEL, AF426405; AAL25086.1;
GO; GO:0004050; F:apyrase activity; IEA.
GO; GO:0004050; F:hydrolase activity; IEA.
PF01150; GDA1_CD39; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 37.6%; Score 1014.5; DB 2; Length Best Local Similarity 41.9%; Pred. No. 3.6e-68; Matches 210; Conservative 90; Mismatches 178; Indels
                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                        Ecto-ATP-diphosphohydrolase (EC 3.6.1.5).
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LAIVAGLVAILL----QCFWK 491
                      ---OCFWK
                                                                                                                                                                                   (TrEMBLrel. 19, C
(TrEMBLrel. 19, I
(TrEMBLrel. 24, I
                                                                                                                                         PRELIMINARY;
| || :::|:
475 LAIVAGLVAILL-
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Search completed: September 21, 2005, 16:21:24 Job time : 94 secs

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; OTHER INFORMATION: Description of Unknown Organism: unknown US-08-930-921-1
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; Sequence 1, Application US/08930921B
; Pattent No. 6287837;
; GENERAL NO. 6287837;
; GENERAL NO. 6287837;
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: BEAUDOIN, ATP-DIPHOSPHOHYDROLASES, PROCESS OF ITILE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PRODUCING THER TITLE OF INVENTION: TECHNOLOGY
; FILE REFERENCE: ATP-DIPHOSPHOHYDROLASES-BEAUDOIN; CURRENT APPLICATION NUMBER: US/08/930,921B
; CURRENT FILING DATE: 1998-01-02
; EARLIER APPLICATION NUMBER: PCT/CA96/00223
; EARLIER FILING DATE: 1996-04-10
; NUMBER OF SEQ. ID NOS: 8
; SOFTWARE: PATENTIN VET. 2.0
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US-10-107-576-14
US-09-905-732B-14
US-09-905-743B-14
US-09-905-744B-15
US-09-905-744B-15
US-10-107-576-15
US-09-905-732B-15
US-09-905-732B-15
US-09-105-112-2
US-09-129-112-15
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     TYPE: PRT
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                                    361 SAFYFVWKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL
                                                                                                                              SILLOGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFL
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APPLICANT: Ford, John
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APPLICANT: Pend, John
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
FILE SPERRENCE: 28110/36457
CURRENT APPLICATION NUMBER: US/09/557,800C
CURRENT FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 1999-00-11
PRIOR PLING DATE: 1999-00-11
PRIOR APPLICATION NUMBER: O9/370,265
PRIOR PLING DATE: 1999-07-09
PRIOR PLING DATE: 1999-07-04
PRIOR PLING DATE: 1999-07-04
PRIOR PLING DATE: 1999-07-04
PRIOR PLING DATE: 1999-07-04
PRIOR PLING DATE: 1999-07-06
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| Sequence 1, Application US/09781796C |
| Sequence 1, Application US/09781796C |
| Patent No. 6800284 |
| GENERAL INFORMATION: |
| APPLICANT: BEAUDOIN, Adrien R. |
| APPLICANT: BEAUDOIN, Adrien R. |
| APPLICANT: BEAUDOIN, Adrien R. |
| APPLICANT: BACH, Fritz H. |
| APPLICANT: ROBSON, Simon |
| TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT |
| TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT |
| TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT |
| TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT |
| FILE REPRENCE: 920333.90019 |
| CURRENT APPLICATION NUMBER: 08/419,204 |
| PRIOR FILING DATE: 1995-04-10 |
| PRIOR FILING DATE: 1996-04-10 |
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| PRIOR FILING DATE: 1998-02-01 |
| PRIOR FILING DATE: 1998-02-01 |
| PRIOR SEQ ID NOS: 8 |
| SOFTWARE: PATENTIN VEF. 2.1 |
| SEQ ID NO 
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                                                                                                                                     SLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFL 480
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                                                                                                    SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL
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                                                                                                                                                                                                                                                                                                                                                           MVLFSLVLFTVAIIGLLIFHKPSYFWKDMV 510
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ORGANISM: Homo sapiens
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Sequence 7977, Application US/09949016

Sequence 7977, Application US/09949016

Batent No. 681239

GENERAL INFORMATION:

APPLICANT: VEWTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT PELICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 2007012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7977

LENGTL.
                                       SLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVPL 480
SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
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43.4%; Score 1171.5; DB 4;
Best Local Similarity 50.3%; Pred. No. 1.9e-115;
Matches 254; Conservative 0; Mismatches 0; I
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                                                                                                                                               MVLFSLVLFTVAIIGLLIFHKP 502
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US-09-949-016-7977
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Patent No. 660032

GENERAL INFORMATION:

APPLICANT: Mulero, Julio

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES

CURRENT APPLICATION NUMBER: US/09/370,625A

CURRENT FILING DATE: 1999-07-16

PRIOR PPLICATION NUMBER: PCT/US99/16180

PRIOR FILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: 09/350,836

PRIOR APPLICATION NUMBER: 09/350,836

PRIOR APPLICATION NUMBER: 09/373,447

PRIOR APPLICATION NUMBER: 09/373,447

PRIOR APPLICATION NUMBER: 09/373,447

PRIOR APPLICATION NUMBER: 09/373,447

PRIOR APPLICATION NUMBER: 09/273,447

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                                                                                                   SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
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                 CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGAF
                                              301 CTKRPEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGAF
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98.2%; Score 2650; DB 4;
Best Local Similarity 100.0%; Pred. No. 7e-272;
Matches 502; Conservative 0; Mismatches 0;
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US-09-370-625A-38
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US-09-370-625A-38
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Patent No. 6759214
GENERAL INFORMATION:
APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Anna Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES
TITLE OF INVENTION: ACIDS
FILE REFERENCE: 28110/36120E
CURRENT APPLICATION NUMBER: US/09/908,510A
CURRENT FILING DATE: 2001-07-13
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39.8%; Pred. No. 1.1e-90;
tive 90; Mismatches 186; Indels
                                                                                         Sequence 4, Application US/09240639;
Patent No. 6350447;
GENERAL INFORMATION:
APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna-Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS REL;
TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACI;
FILE REPERENCE: 9588-066
CURRENT APPLICATION NUMBER: US/09/240,639;
CURRENT PILING DATE: 1998-01-29;
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 94
Best Local Similarity 39.89
Matches 191; Conservative
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US-09-908-510A-4
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APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Anna Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND 1TITLE OF INVENTION: ACIDS
FILE REFERENCE: 28110/36120A
CURRENT APPLICATION NUMBER: US/09/905,744B
RICH APPLICATION NUMBER: 09/240,639
PRIOR FILING DATE: 1999-01-29
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PRIOR APPLICATION NUMBER: 09/240,639 PRIOR FILING DATE: 1999-01-29 NUMBER OF SEQ ID NOS: 32 SOFTWARE: PatentIn version 3.1 SEQ ID NO 4 LENGTH: 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09905744B Patent No. 6780410 GENERAL INFORMATION:
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SEQ ID NO 4
LENGTH: 529
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ORGANISM: Homo Sapiens
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US-09-908-510A-4
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Sequence 4, Application US/10107576

Sequence 4, Application US/10107576

Patent No. 6783959

GENERAL INFORMATION:
APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND TITLE OF INVENTION: WOMBER: US/10/10/576

FILE REFERENCE: 28110/36120H
CURRENT APPLICATION NUMBER: US/10/10/576

CURRENT FILING DATE: 12002-03-27

PRIOR APPLICATION NUMBER: 09/240,639

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PatentIn version 3.1
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Best Local Similarity 39.8%
Matches 191; Conservative
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US-10-107-576-4
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381 KVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFI
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Patent No. 6780977

GENERAL INFORMATION:
APPLICANT: Chadwick, Brian Paul
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
FILE REFERENCE: 9598-066
CURRENT APPLICATION NUMBER: US/10/107,660
CURRENT FILING DATE: 1998-01-29
PRIOR PILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 4
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ORGANISM: Homo sapiens
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US-10-107-660-4
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39.8%;
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Matches 191; Conservative
CURRENT FILING DATE: 2001
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.
SEQ ID NO 4
LENGTH: 529
                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-949-016-6049
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ORGANISM:
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                                                                                                   Sequence 4, Application US/09905732B

Sequence 4, Application US/09905732B

PARENT No. 678732B

GENERAL INFORMATION:
APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
TITLE OF INVENTION: NUMBER: US/09/905, 732B
CURRENT APPLICATION NUMBER: US/09/905, 732B
CURRENT APPLICATION NUMBER: 09/240, 639
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 529
     441 GKIQGSDAGWTIGYMLNLTNMIPAEQPL-STPLSHSTYVFLMVLFSLVLFTVAIIGLLIF 499
                      85 RVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEEL 144
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APPLICANT: JIANG, FENG
TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS
FILE REFERENCE: UTSC: 6580S
CURRENT APPLICATION NUMBER: US/09/923,304
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; Pred. No. 1.1e-90;
90; Mismatches 186; Indels
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39.8%;
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Best Local Similarity 39.8'
Matches 191; Conservative
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                                                                                     RESULT 11
US-09-905-732B-4
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US-09-923-304-4
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Sequence 6049, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
SPRIOR FILING DATE: 2000-10-03
SEQUID NOS: 207012
SOFTWARE: FRAESEQ FOF WINDOWS VERSION 4.0
SEQUID NO 6049
                                                                                                                                                                                                                                        85 RVKGPGISKPVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEEL 144
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Length 529;
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      DB 4;
   34.9%; Score 942.5; DB 4;
39.8%; Pred. No. 1.1e-90;
tive 90; Mismatches 186;
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Pred. No. 1.1e-90;
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Sequence 11328, Application US/09949016
Facent No. 681239
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: 05/949,016
CURRENT PILING DATE: 2000-00-41
FRICH FILING DATE: 2000-10-20
FRICH FILING DATE: 2000-10-03
FRICH REPLICATION NUMBER: 60/231,768
FRICH REPLICATION NUMBER: 60/231,498
FRICH RELING DATE: 2000-10-03
FRICH REPLICATION NUMBER: 60/231,498
FRICH RELING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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Best Local Similarity 39.64
Matches 190; Conservative
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APPLICANT: Chadwick, Brian Paul
APPLICANT: Crischauf, Anna Maria
APPLICANT: Frischauf, Anna Maria
APPLICANT: Frischauf, Anna Maria
APPLICANT: Frischauf, Anna Maria
APPLICANT: BRIANDS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS
FILE REFERENCE: 28110/36120C
CURRENT APPLICATION NUMBER: 09/240,639
RIOR APPLICATION NUMBER: 09/240,639
RIOR APPLICATION NUMBER: 09/240,639
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
   7;
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                                                                                                 RVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEEL 144
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39.8%; Pred. No. 1.1e-90;
tive 90; Mismatches 186;
Mismatches 186;
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90;
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Best Local Similarity 39.8%,
Matches 191; Conservative
Conservative
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ORGANISM: Homo Sapiens
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US-09-905-743B-4
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Search completed: September 21, 2005, 16:22:30 Job time: 30 secs

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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 30, Appl	Sequence 2, Appli	Sequence 297, App	Sequence 97, Appl	Sequence 38, Appl	Sequence 27, Appl	Sequence 2, Appli	Sequence 6, Appli
ΩI	US-09-835-147-2	US-09-374-586-1	US-09-781-796B-1	US-10-646-308-30	US-10-922-378-2	US-10-934-998-297	US-10-934-998-97	US-10-092-063-38	US-09-835-147-27	US-09-374-586-2	US-09-835-147-6
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Sequence 2, Application US/09835147

Patent No. US2002002277A1

General INFORMATION:

APPLICANT Maliszewski, Charles R.

APPLICANT Maliszewski, Charles R.

APPLICANT Gimpel, Stewn D.

TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE REFERENCE: 2879-US

CURRENT APPLICATION NUMBER: US/09/835,147

CURRENT APPLICATION NUMBER: US 60/104,585

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1999-11-06

PRIOR FILING DATE: 1999-08-13

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PATENTIN OF 2

LENGTH: 510

TYPE: PRT

ORGANISM: Homo sapiens

US-09-035-147-2

Query Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps
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GENERAL INFORMATION

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GENERAL INFORMATION

APPLICANT: BRAUDOIN, Adrien R.

APPLICANT: BACH, Fritz H.

APPLICANT: BACH, Fritz H.

APPLICANT: ROBSON, Simon

TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT

TITLE OF INVENTION: TECHNOLOGY

TITLE OF INVENTION WIMBER: US/09/781,796B

CURRENT FILING DATE: 1995-04-10

PRIOR FILING DATE: 1995-04-10

PRIOR PILING DATE: 1996-04-10

PRIOR FILING DATE: 1998-02-01

WUMBER OF SEQ ID NOS: 8

SOFTWARE: PATCHTIN VET: 2.1

SEQ ID NO 1
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181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFR 240
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100.0%; Score 2698; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.3e-233;
Matches 510; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                   MVLFSLVLFTVAIIGLLIFHKPSYFWKDMV 510
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Patent No. US20020138858A1
RENERAL INFORMATION:
APPLICANT: PINSKy.
TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND TITLE OF INVENTION: LSCHEMIC DISORDERS
TITLE OF INVENTION: ISCHEMIC DISORDERS
TITLE REFERENCE: 057/59167
CURRENT APPLICATION NUMBER: US/09/374,586
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO
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Best Local Similarity 100.0%; Pred. No. 1.3e-233;
Matches 510; Conservative 0; Mismatches 0; Indels 0
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TYPE: PRT
ORGANISM: HOMO-SAPIEN
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Sequence 2, Application US/10922378

Publ.dcation No. US20050169968A1

Publ.dcation No. US20050169968A1

APPLICANT: ELMALEH, DAVID R.

APPLICANT: ELMALEH, DAVID R.

APPLICANT: PAPISOV, MIKHAIL L.

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: UMBER: US/10/922,378

CURRENT APPLICATION NUMBER: US/10/922,378

CURRENT FILING DATE: 2004-08-19

PRIOR PLING DATE: 2003-02-19

PRIOR FILING DATE: 2002-02-19

PRIOR FILING DATE: 2002-02-20

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PATENTIN Ver. 3.3

SOFTWARE: PATENTIN Ver. 3.3
                                       SLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLGHSTYVFL 480
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100.0%; Score 2698; DB 18;
Best Local Similarity 100.0%; Pred. No. 1.3e-233;
Matches 510; Conservative 0; Mismatches 0;
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CTKRFEMTLPFQQFE1QG1GNYQQCHQS1LELFNTSYCPYSQCAFNG1FLPPLQGDFGAF
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                                                                                                                                                                                                                                                                                                                                                                             Sequence 30. Application US/10646308

Sequence 30. Application US/10646308

Bublication No. US20040136992A1

GENERAL INFORMATION:

APPLICANT: BURTON, Paul B. J.

APPLICANT: DEISHER, Theresa A.

TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR FILE REPERENCE: 3432-B

CURRENT APPLICATION NUMBER: US/10/646,308

CURRENT FILING DATE: 2003-08-21

PRIOR APPLICATION NUMBER: --to be assigned---
PRIOR PILING DATE: 2003-08-12

PRIOR PILING DATE: 2003-08-12

PRIOR FILING DATE: 2003-08-12

PRIOR FILING DATE: 2003-08-13

SOFTWARE: PATENTION NUMBER: 60/406,418

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PATENTIN Version 3.2

LENGTH: 510

TYPE: BRT

CRANISM: Homo sapiens

US-10-646-308-30
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485 SLVLFTVAIIGLLIFHKPSYFWKDMV 510
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                                                  Sequence 97, Application US/10934998
Publication No. US20050153917A1
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-10-092-063-38
                                   US-10-934-998-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-934-998-97
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                                                                                                                                                 APPLICANT: AL-MAHMOOD, SALMAN
APPLICANT: AL-MAHMOOD, SALMAN
APPLICANT: AL-MAHMOOD, SALMAN
APPLICANT: AL-MAHMOOD, SALMAN
APPLICANT: ACININ SYLVIE
APPLICANT: COLIN, SYLVIE
TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL
TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF
TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF
CURRENT APPLICATION NUMBER: US/10/934,998
CURRENT FILING DATE: 2004-09-03
PRIOR PILING DATE: 2003-03-04
PRIOR FILING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PALENTIN VERSION 3.2
SEQ ID NO 297
LENGTH: 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
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100.0%; Pred. No. 1.3e-233;
tive 0; Mismatches 0;
MVLFSLVLFTVAIIGLLIFHKPSYFWKDMV 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 510; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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| FUDITICATION NO. US20050153917A1
| GENERAL INFORMATION, SALMAN
| APPLICANT: AL-MAHMOOD, SALMAN
| APPLICANT: AL-MAHMOOD, SALMAN
| APPLICANT: COLIN, SYLVIE
| APPLICANT: COLIN, SYLVIE
| APPLICANT: COLIN, SYLVIE
| TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL
| TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF
| FILE REFREENCE: BMA-04-1206
| CURRENT APPLICATION NUMBER: US/10/934, 998
| CURRENT PILING DATE: 2004-09-03
| PRIOR PILING DATE: 2003-03-04
| PRIOR FILING DATE: 2002-04-11
| NUMBER OF SEQ ID NOS: 301
| SOFTWARE: PATENTIN VERSION 3.2
| SEQ ID NO 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 PVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINY 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 FEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGAFSAFY 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: CDS protein of the sequence GS-N45: 184..1737 (GS-P45)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 DYNVYTHSFLCYGKDQALMQKLAKDIQVASNEILKDPCFHPGYKKVVNVSDLYKTPCTKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312 FEMTLPPQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGAFSAFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 FVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             425 QGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFLMVLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 YKWPAEKENDTGVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 99.2%; Score 2677; DB 18; Length 517; Best Local Similarity 100.0%; Pred. No. 1e-231; Matches 506; Conservative 0; Mismatches 0; Indels 0
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CRVKGPGISKPVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEE 143
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                    Sequence 27, Application US/09835147

Patent No. US20020002277A1

GENERAL INFORMATION

**APPLICANT: Maliazewski, Charles R.

APPLICANT: Maliazewski, Charles R.

APPLICANT: Gayle III, Richard B.

TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE REFERENCE: 2879-US

CURRENT APPLICATION NUMBER: US/09/835,147

CURRENT APPLICATION NUMBER: US 60/104,585

PRIOR PLING DATE: 1998-10-16

PRIOR FLING DATE: 1998-10-16

PRIOR FLING DATE: 1999-08-13

PRIOR FLING DATE: 1999-08-13

**PRIOR FLING DATE: 1999-08-13

**PRIOR FLING DATE: 1999-08-13

**PRIOR PLING DATE: 1999-08-13

**PRIOR 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 SSIIAVIALLAVGLTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 NNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQALW
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER TAP-SEMATION: construct of human CD39
US-09-835-147-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 87.4%; Score 2358; DB 9; Best Local Similarity 97.8%; Pred. No. 4.5e-203; Matches 443; Conservative 2; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           444 QGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHST 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-09-374-586-2
, Sequence 2, Application US/09374586
, Parent No. US20020138858A1
, GENERAL INFORMATION:
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                                                                                                                 APPLICANT: MULERO, JULIO
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
FILE REFERENCE: 2810/385908
CURRENT APPLICATION NUMBER: US/10/092,063
CURRENT PELING DATE: 2002-03-05
FRIOR APPLICATION NUMBER: 09/370,265
FRIOR APPLICATION NUMBER: 09/370,265
FRIOR APPLICATION NUMBER: 09/370,265
FRIOR APPLICATION NUMBER: 09/350,836
FRIOR APPLICATION NUMBER: 09/350,836
FRIOR PELING DATE: 1999-07-09
FRIOR PELING DATE: 1999-07-09
FRIOR PELING DATE: 1999-07-04
FRIOR APPLICATION NUMBER: 09/244,444
FRIOR APPLICATION NUMBER: 09/244,444
FRIOR APPLICATION NUMBER: 09/122,449
FRIOR APPLICATION NUMBER: 09/122,449
FRIOR APPLICATION NUMBER: 09/118,205
FRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 HQETPVYLGATAGWRLLRMESEELADRVLDVVERSLSNYPFDFQGARIJTGQEEGAYGWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 TINYLLGKFSQKTRWFSIVPYETINNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 98.2%; Score 2650; DB 13; Best Local Similarity 100.0%; Pred. No. 2.7e-229; Matches 502; Conservative 0; Mismatches 0;
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Publication No. US20020173005A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-10-092-063-38
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LENGTH: 502
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APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Gayle III, Richard B.
APPLICANT: Gayle III, Richard B.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147
CURRENT FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
PRIOR PLILING DATE: 1998-10-16
PRIOR PLILING DATE: 1998-10-06
PRIOR PLILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 31
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APPLICANT: Pinsky, David J.
TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND TITLE OF INVENTION: 1SCHEMIC DISORDERS
FILE REFERENCE: 0575/59167
CURRENT APPLICATION NUMBER: US/09/374,586
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 439
TYPE: PRT
TYPE: PRT
CREANIEM: Homo sapiens
ORGANIEM: Homo sapiens
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100.0%; Pred. No. 3.3e-202;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 439; Conservative
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Sequence 30, Application US/09835147

Patent No. US2002002277a1

GENERAL INFORMATION:

APPLICANT: Maliszewski, Charles R.

APPLICANT: Maliszewski, Charles R.

APPLICANT: Gaple III, Richard B.

APPLICANT: Gimpel, Steven D.

TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE REFERENCE: 2979-US

CURRENT APPLICATION NUMBER: US/09/835,147

CURRENT APPLICATION NUMBER: US 60/104,585

PRIOR REPLICATION NUMBER: US 60/104,666

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

PRIOR PLILOR DATE: 1999-10-13

PRIOR PLILOR DATE: 1999-10-13

PRIOR FILING DATE: 1999-10-13

PRIOR PELICATION NUMBER: US 60/149,010

PRIOR PELICATION NUMBER: PCT/US99/22955

PRIOR PELICATION NUMBER: PCT/US99/22955

PRIOR FILING DATE: 1999-10-13

WUMBER OF FILING DATE: 1999-10-13

PRIOR FILING DATE: 1999-10-13

PRIOR PELICATION NUMBER: PCT/US99/22955

PRIOR FILING DATE: 1999-10-13

PRIOR PLILOR DATE: 1999-10-13

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                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Pusion
OTHER INFORMATION: construct of human CD39
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87.0%; Score 2348; DB 9; L
Best Local Similarity 100.0%; Pred. No. 3.4e-202;
Matches 439; Conservative 0; Mismatches 0;
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 454
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APPLICANT: Gayle III, Richard B.
APPLICANT: Gayle III, Richard B.
APPLICANT: Drice, Virginia L.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE RERERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147
CURRENT FILING DATE: 2001-04-13
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/109, 466
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
NUMBER: OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                       35 TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQK
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                                                                                                                                            38 TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQK
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                                                87.0%; Score 2348; DB 9; L
100.0%; Pred. No. 3.7e-202;
tive 0; Mismatches 0;
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100.0%; Pred. No. 3.7e-202;
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                                                Query Match
Best Local Similarity 100.
Matches 439; Conservative
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       US-09-835-147-29
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LENGTH: 474
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Sequence 29, Application US/09835147

Sequence 29, Application US/02002077A1

GENERAL INFORMATION:

APPLICANT: Galpel III, Richard B.

APPLICANT: Gimpl. Steven D.

APPLICANT: Gimpl. Steven D.

TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE REFERENCE: 2879-US

CURRENT APPLICATION NUMBER: US/09/835,147

CURRENT FILING DATE: 2001-04-13

PRIOR PILING DATE: 1998-10-16

PRIOR FILING DATE: 1998-11-06

PRIOR APPLICATION NUMBER: US 60/107,466

PRIOR APPLICATION NUMBER: US 60/149,010

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 1999-10-13

SOFTWARE: PATCH NUMBER: PCT/US99/22955

PRIOR FILING DATE: 1999-10-13

SEQ ID NO 29

LEMERTH: AT3
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion
OTHER INFORMATION: construct of human CD39
                                                  Fusion
                                                                                                                                            Length 463
                                                                                                                                                                                     Indels
                                              OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: construct of human CD39
                                                                                                                                       Query Match

87.0%; Score 2348; DB 9; L
Best Local Similarity 100.0%; Pred. No. 3.5e-202;
Matches 439; Conservative 0; Mismatches 0;
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US-09-835-147-30
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US-09-835-147-29
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Sequence 3, Application US/09835147

Sequence No. US20020002277A1

GENERAL INFORMATION:

APPLICANT: Maiszewski, Charles R.

APPLICANT: Galmel, Steven B.

APPLICANT: Price, Virginia L.

APPLICANT: Gimpel, Steven D.

TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE REFERENCE: 2979-US

CURRENT APPLICATION NUMBER: US/09/835,147

CURRENT APPLICATION NUMBER: US 60/104,585

PRIOR FILING DATE: 1998-110-16

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-10-13

SPIOR PILING DATE: 1999-10-13

SPIOR PILING DATE: 1999-10-13

SPIOR PILING DATE: 1999-10-13

SEQUID NOS: 31

                                                                                                                                             STQVTFVPQNQTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEI
                                         TQNKALPENVKYGI VLDAGSSHTSLY I YKWPAEKENDTGVVHQVEECRVKGPGI SKFVQK
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                          TONKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHOVEECRVKGPGISKFVOK
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Mismatches
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ORGANISM: Artificial Sequence
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38 TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQK 97
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                                                                                VNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSLS
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BD228699.1 GI:33038469

BD228689.1 GI:33038469

Synthetic construct
Synthetic construct
other sequences; artificial sequences.

Chases 1 to 1365)

Maliszewski,C.R., Iii,R.B.G., Price,V.L. and Gimpe,S.D.
Inhibitors of platelet activation and recruitment
Datent: JP 2002527096-A 2 27-AUG-2002;
IMMUNEX CORP
OS Artificial Sequence
PD 27-AUG-2002
PP 13-AUG-2002
PP 13-AUG-1999 US 60/104585,06-NOV-1998 US 60/107466 PR
13-AUG-1999 US 60/149010
PP CHARLES R MALISZEWSKI,RICHARD B GAYLE III,VIRGINIA L PRICE, PI
AP037366 Mus muscu BC011278 Mus muscu UB1295 Rattus norv CQ870265 Sequence AF05940 Bos tauru CQ870268 Sequence AJ13134 Homo sapi AX828501 Sequence AS073267 Xenopus 1 BC0751824 Sequence AJ73169 Gallus ga BC078240 Danio rer CQ71525 Sequence AR187035 Sequence AR567207 Sequence AR567427 Mus muscu BC031143 Mus muscu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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Inhibitors of platelet activation and recruitment.
BD228699
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                      CQ870265
CQ870268
CQ870268
HSA133134
AX828501
AX828501
AX828517
CQ721824
CQ721824
AJ720369
BC07662
CQ715235
AR194793
AR567109
AR567109
AR567207
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AR567917
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AF039817
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BC031143
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C12N5/10,
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TITLE
JOURNAL
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BD228699
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BD228700 Inhibitor
BD228698 Inhibitor
BD228698 Inhibitor
U87967 Human ATP d
AR168353 Sequence
AR380930 Sequence
AR3828644 Sequence
S73813 CD3=1ympho
AR828400 Sequence
CQ870272 Sequence
CQ870275 Sequence
CQ870276 Sequence
                                                                                   5 ; Search time 6123.5 Seconds (without alignments) 10801.234 Million cell updates/sec
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                                                                                                                                                            Description
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                      September 21, 2005, 16:22:35
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Maximum Match 100%
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                                 GGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTTCTGGTACCTACATTCTCTCCCTC 1200
                                                      CTTCTGCAAGGCTATCATTTCACAGCTGATTCCTGGGAGCACATCCATTTCATTGGCAAG 1260
                                                                                                                             CTTCTGCAAGGCTATCATTCACAGCTGATTCCTGGGAGCACATCCATTTCATTGGCAAG 1260
                                                                                                                                                                              ATCCAGGGCAGCGACGCCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATC 1320
                                                                                                                                                                                                     1261 ATCCAGGGCAGCGAGCGCCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAAGATG 1320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 GCACCTACTICAAGTICTACAAAGAAAACACAGCTAACTAGTICAACCCAGAACAAAGCA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTCAGAAAGTAAATGAAATAGGC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OS Artificial Sequence
PN JP 2002527096-A/3
PD 27-AUG-2002
PP 13-OCT-1999 JP 2000577185
PR 16-OCT-1999 US 60/104585,06-NOV-1998 US 60/107466 PR
13-AUG-1999 US 60/149010
PI CHARLES R MALISZEWSKI, RICHARD B GAYLE III, VIRGINIA L PRICE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STEVEN D GIMPEL C12N15/09,A61K38/00,A61P9/00,C07K14/705,C12N1/15,C12N1/19,
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JP 2002527096-A/3.
synthetic construct
synthetic construct
other sequences, artificial sequences.
1 (bases 1 to 1437)
Maliazewski,C.R., Iii,R.B.G., Price,V.L. and Gimpe,S.D.
Inhibitors of platelet activation and recruitment
Patent: JP 2002527096-A 3 27-AUG-2002;
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                                                                                                                                                                                                                                                    CCAGCTGAGCAATGTCCACACCTCTCTCCCACTCCACTA 1365
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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100.0%; Score 1365;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1365; Conservative 0; Mismatches
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                                                                                                                             TACATCTATAAGTGGCCAGCAGAAAGGAGAATGACACAGGCGTGGTGCATCAAGTAGAA 180
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ATTTACCTGACTGGATTGCATGGAAAGAGCTAGGGAAGTGATTCCAAGGTCCCAGCACCAA
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DESCRIPTION OF A PRICE        1333 ATCCAGGGCAGCGACGCCGGCTGGACTTTGGGCTACATGCTGAACCTGACCACACATGATC 1392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC C12N15/09, AblAssvvv...-C12N5/10, C12N5/10, C12N5/10, PC C12P21/02//C12N9/14, C12N15/00, A61K37/02, C12N5/00 CC Description of Artificial Sequence: Fusion construct of human CD39
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synthetic construct
other sequences, artificial sequences.

1 (bases I vol 1464)
Maliszewski, C.R., Iii, R.B.G., Price, V.L. and Gimpe, S.D.
Inhibitors of platelet activation and recruitment
Patent: JP 2002527096-A 13 27-AUG-2002;
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                                          Inhibitors of platelet activation and recruitment. BD228710 BD228710 IG:33038480 BD228710.1 GI:33038480 BD20552796-A/13.
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherita; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1599)
Maliszewski,C.R., Iii,R.B.G., Price,V.L. and Gimpe,S.D.
Inhibitors of platelet activation and recruitment
Patent: JP 2002527096-A 1 27-AUG-2002;
IMMUNEX CORP
                                                                                                                                                OS HOMO sepiens (human)
PN JP 2002527096-A/1
PN JP 2002527096-A/1
PD 27-A04G-2002
PP 13-OCT-1999 JP 2000577185
PR 16-OCT-1999 US 60/104585,06-NOV-1998 US 60/107466 PR 13-A0G-1999 US 60/149010
PI CHARLES R MALISZEWSKI, RICHARD B GAYLE III, VIRGINIA L PRICE, STEVEN D GIMPEL
PL C12015/09, A61K38/00, A61P9/00, C07K14/705, C12N1/15, C12N1/19, P
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Location/Qualifiers

    1599
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

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Best Local Similarity 99.8%;
Matches 1321; Conservative (
                           Homo sapiens (human)
Homo sapiens
  BD228698.1 GI:330
JP 2002527096-A/1
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PAT 17-JUL-2003

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Kaczmarek, E., Koziak, K., Sevigny, J., Siegel, J.B., Anrather, J., Beaudoin, A.R., Bach, F.H. and Robson, S.C.

Birect Submission

Submitted (30-JAN-1997) Medicine, Harvard University, 99 Brookline Avenue, BIDMC, RN., Boston, MA 02215, USA

Location/Qualifiers
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Raczmarek, E., Koziak, K., Sevigny, J., Siegel, J.B., Anrather, J., Beaudoin, A.R., Bach, F.H. and Robson, S.C. Identification and characterization of CD39/vascular ATP
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Beaudoin, A.R. and Sevigny, J.
Mammalian ATP-diphosphohydrolases and process of purification
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Patent: US 6287837-A 2 11-SEP-2001;
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1. .1818
/organism="unknown"
/mol_type="unassigned DNA"
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1818)
Maliazewski, C. R., Delespesse, G.J., Schoenborn, M.A., Armitage, R.J.,
Fanslow, W.C., Nakajima, T., Baker, E., Sutherland, G.R.,
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            714 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCAGACTATGGAGTCCCCAGATAATG
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Genes involved in regulating angiogenesis, pharmaceutical
preparations containing same and applications thereof
Patent: WO 01074013-A 290 12-SEP-2003;
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/mol_type="unassigned DNA"
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TOTTPVPQNOTIESPUNALGPRLYGKDYNVTTHSFLCYGKDALMQCARG
TLRDBCFHPGYKKVNNSDLYRTPCTKRFEWTLPFQDFBLQGIGNYQQCHQSILELER
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The CD39 lymphoid cell activation antigen. Molecular cloning and etructural characterization
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entry [NCBI gibbsq 156681] from the original journal article.
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                               /product="lymphoid cell a
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                                                                                                                                                                                                                                                                /gene="CD39"
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diphosphatase homolog"
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Titani,K., Fujimura,Y. and Narita,N.
The cDNA cloning of human placental ecto-ATP diphosphohydrolases I
and II
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                  AAGTCTCTCAGGAAAAGGTGACTGAGATGAAAAAGTTCTGTGCTCAGCCTTGGGAGG
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                                                                                        1001 ATTTTGGGGCATTTTCAGCTTTTTACTTTGTGATGAAGTTTTTAAACTTTGACATCAGAGA
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Submitted (23-FEB-1999) Matsumoto M., Department of Blood
Transfusion Medicine, Nara Medical University, Kashihara,
Nara,634-8522, JAPAN
Location/Qualifiers
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/organism="Homo sapiens"
/nol_type="mRNA"
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1. .2081
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184. 1737
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Matsumoto, M.
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Genes involved in regulating angiogenesis, pharmaceutical preparations containing same and applications thereof Patent: WO 0374073-A 46 12-SEP-2003; Gene Signal (FR)
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                                                                                                                                        GTTACTGCCCTTACTCCCAGTGTGCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGG
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                                                                        TCCAGGGTATTGGAAACTATCAACAATGCCATCAAAGCATCCTGGAGCTCTTCAACACA
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Novel therapeutic targets in cancer
Patent: WO 20040/73120-A 693 02-SEP-2004;
Sagres Discovery, Inc. (US)
Location/Qualifiers
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    /organism="Homo sapiens"
/mol_type="unassigned DNI
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MKKFCAQPWESIKTSYGVKEKYLSFYCFSGTYILSLLLQGYHFTADSWEHIHPIGKI
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Patent: WO 2004074320-A 691 02-SEP-2004;
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Location/Qualifiers
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/mol_type="unassigned DNA"
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       TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTTGGACCTTTGGGG
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/note= "Coding region of human soluble CD39 (solCD39)"
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                                                                                                                                                                                     New soluble CD39 polypeptides having apyrase activity, useful for inhibiting angiogenesis and treating unstable angina, myocardial infarction, stroke, coronary artery disease or injury.
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100.0%; Score 1365; DB 3; Length 1365;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1365; Conservative 0; Mismatches 0; Indels 0;
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                            (IMMV ) IMMUNEX CORP
                                                                                                                       WPI; 2000-339644/29
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                                                                         Maliszewski CR,
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The present cDNA sequence is a fusion construct encoding sol(soluble) CD39 having apyrase activity. Fusion of 12 amino acids from the N-terminus of mature human LI2 to the solCD39 coding region results in high levels of both expression and activity in the supernatants of transfected cells. This is used in the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atheroselerosis, peripheral vascular occlusion, preeclampsia, embolism, platelet-associated ischaemic sischaemia, a thrombosia, embolism, platelet-associated ischaemic ischaemia, a thrombosis, including occonary attery thrombosis, cerebral attery thrombosis, including cononary attery thrombosis, thrombosis, coagulopathy, deep venous thrombosis (bur), pulmonary embolism (PE), transfent ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood
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cerebral ischaemia; thrombotic disorder; coronary artery thrombosis; cerebral artery thrombosis; intracardiac thrombosis; wenous thrombosis; peripheral artery thrombosis; coagulopathy; deep venous thrombosis; PE; pulmonary embolism; transient ischaemic attack; thrombus formation; PE; pulmonary embolism; transient ischaemic attack; thrombus formation; occlusion; reenosis; restenosis; antianginal; cardiant; cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant; coronary ischaemia; vascular occlusion; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting platelet activation and recruitment, useful for treating a mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD39 polypeptides.
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1020 1200 1260 300 420 480 480 540 540 GAGTIGGCAGACAGGGTICTGGATGTGGTGGAGAGGAGCCTCAGCAACTACCCCTTTGAC 420 600 600 999 660 720 720 780 780 840 840 900 900 960 960 GAGACACCCGTTTACCTGGGAGCCACGGCAGGCATGCGGTTGCTCAGGATGGAAAGTGAA GAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTCAGAAAGTAAATGAAAATAAGGC **ATTTACCTGACTGATTGCATGGAAAGAGCTAGGGAAGTGATTCCAAGGTCCCAGCACCAA** GAGACACCCGTTTACCTGGGAGCCACGCCAGGCATGCGGTTGCTCAGGATGGAAAGTGAA GAGTTGGCAGACAGGGTTCTGGATGTGGGAGAGAGCCTCAGCAACTACCCCTTTGAC Trocadegracicatracresceaagaagaagarecrarescresarracrare AACTATCTGCTGGGCAAATTCAGTCAGAAAACAAGGTGGTTCAGCATAGGAA AACTATCTGCTGGGGAAATTCAGTCAGAAAACAAGGTGGTTCAGCATAGTCCCATATGAA TTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATGCTCTGCAATTTCGCCTCTAT TITCATCCTGGATATAAGAAGGTAGTGAACGTAAGTGACCTTTACAAGACCCCTGCACC CTTCTGCAAGGCTATCATTTCACAGCTGATTCCTGGGAGCACATCCATTTCATTGGCAAG TTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGAAGGTGCCTATGGCTGGATTACTATC **ACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTGGGGGGAGCCTCTACACAAGTCACT** TITIGIACCCCAAAACCAGACTATCGAGTCCCCAGATAATGCTCTGCAATTTCGCCTCTAT GGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGCTATGGGAAGGATCAGGCACTC TGGCAGAAACTGGCCAAGGACATTCAGGTTGCAAGTAATGAAATTCTCAGGGACCCATGC TTTCATCCTGGATATAAGAAGGTAGTGAACGTAAGTGACCTTTACAAGACCCCTGCACC **AAGAGATTTGAGATGACTCTTCCATTCCAGCAGTTTGAAATCCAGGGTATTGGAAACTAT** 841 AAGAGATTTGAGATGACTCTTCCATTCCAGCAGTTTGAAATCCAGGGTATTGGAAACTAT CAACAATGCCATCAAAGCATCCTGGAGCTCTTCAACACAGTTACTGCCCTTACTCCCAG caacaargccarcaaagcarccrogagcrcrrcaacaccagrracroccrracrccag TGTGCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGGATTTTGGGGCATTTTCAGCT TTTTACTTTGTGATGAAGTTTTTAAACTTGACATCAGAAAAGTCTCTCAGGAAAAGGTG GGAGTAAAAGGAGAAGTACCTGAGTGAATACTGCTTTTTCTGGTACCTACATTCTCTCCCTC GGCAAGGACTACAATGTCTACACATAGCTTCTTGTGCTATGGGAAGGATCAGGCACTC TGGCAGAAACTGGCCAAGGACATTCAGGTTGCAAGTAATGAAATTCTCAGGGACCCATGC TGTGCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGGATTTTGGGGCATTTTCAGCT 1081 ACTGAGATGATGAAAAGTTCTGTGCTCAGCCTTGGGAGGAGATAAAAACATCTTACGCT GGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTTTCTGGTACCTACATTCTCCCTC 181 241 181 241 301 361 421 481 481 541 301 361 421 541 601 781 601 199 199 721 721 781 841 901 901 961 961 1021 1021 1081 1141 1141 1201 1201 8 셤 ò 셤 ò 요 ð 뭐 ò 셤 à 셤 ઠે g ð 셤 g 셤 g Š à ò g 셤 g ò ò ઠે 셤 ઠે 셤 ò 셤 à ò

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cc mature N-terminus of hIL2 and soluble CD39 (solCD39) coding region, having apyrase activity. This produces high levels of solCD39 expression and activity in the transfected cells. Soluble CD39 is constructed by removing the N- and C-terminal transmembrane domains. It retains the capacity to metabolise ATP and ADP at relevant concentrations and the ability to block and reverse ADP-induced platelet activation and concentrations and the ability to block and reverse ADP-induced platelet activation and concentrations and the ability to block and reverse ADP-induced platelet activation and constant and reverse ADP-induced platelet activation and constable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vacular occlusion, precelampsia, corinity, atherosclerosis, peripheral vacular occlusion, precelampsia, coronary and cerebral ischaemia, thrombocit disorders including lung, coronary and cerebral artery thrombosis, intracardiac and venous thrombosis, coagulopathy, deep venous thrombosis (DVF), pulmonary embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, corrected to the preventing thrombus formation or reformation, occlusion, reocclusion, corrected to the coronary activated to the coronary activated to the coronary activated thrombosis of blood vessels or stroke
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/note= "Coding region of human soluble CD39 (solCD39)"
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                                                                                     CCAGCTGAGCAACCATTGTCCACACCTCTCCCCACTCCACCTAA 1365
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The present sequence is coding region of pIL2SolCD39, a fusion construct encoding sol (soluble) CD39 having apyrase activity. Fusion of 12 amino acids from the N-terminus of mature human IL2 to the solCD39 coding region results in high levels of both expression and activity in the supernatants of transfected cells. This is used in the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, platelet-associated ischaemic disorder including lung coronary artery thrombosis, cerebral ischaemia, thrombotic disorder including coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous thrombosis, venous thrombosis, thrombosis, pransition careformation, collusion, reocclusion, stenois or restenosis of blood vessels or stroke
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 TTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGCGGGTTCTTCTCACACAAGTTTA
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ive 0; Mismatches
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Soluble CD39; solCD39; human; apyrase activity; platelet activation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombus formation; occlusion; restenosis; angiogenesis; antianginal; cerebroprotective; antiateriosclerotic; anticoagulant; cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mature human interleukin 2 N-terminal end"
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/product= "Fusion protein of pIL2LFlagSolCD39"
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                                                                                                                                                                                                                    Human soluble CD39 fusion DNA construct, pIL2LFlagSolCD39.
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acids from the mature N-terminus of hIL2, a linker, FLAG tag sequence and soluble CD39 (solCD39) coding region, that has apyrase activity. This produces high levels of solCD39 expression and activity in the transmembrane domains. It retains the capacity to metabolise ATP cerminal transmembrane domains. It retains the capacity to metabolise ATP concentrations and the ability to Diock and reverse ADP-induced platelet activation and recruitment, including platelet aggregation. Soluble CD39 polypeptides are useful for inhibiting considerations and recruitment including platelet aggregation. Struke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, precediampsia, embolism, creatment of schaemia, thrombotic disorders including lung, coronary and cerebral ischaemia, thrombosis, intracardiac and venous thrombosis, capacity, pulmonary embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, reocclusion, stenosis or restenosis of blood vessels or stroke
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibiting platelet activation and recruitment, useful for treating a mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD39 polypeptides.
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/product= "Mature human IL2"
/note= "First N-terminal 12 amino acids"
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/note= "huIL2 leader sequence"
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Best Local Similarity 98.5%;
Matches 1334; Conservative
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P-PSDB; AAY70898.
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                      1429
                                                                                                                                                                                                                           Soluble CD39; human, apyrase activity; platelet activation; inhibitor; unstable angina; myocardial infarction; erroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombos formation; occlusion; stenosis; restenosis; angiogenesis; antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant; cardiant; vasotropic; thrombolytic; ss.
                    1370 GCGACGCCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATCCCAGCTGAGC
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/note= "Cell surface molecule"
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                      preventing thrombus formation or reformation, occlusion, reocclusion,
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                                                                                                                                          Length 1599;
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Matches 1321; Conservative
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GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCCCAGATAATG 772
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                P-PSDB; AAY70887
                                                             polypeptides.
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                 1301 TGAACCTGACCAACATGATCCCAGCTGAGCAACCATTGTCCACACCTCTCTCCCACTTCCA 1360
                                                                                                                                                                                                                                                                                                                                                              Soluble CD39; ADP-induced platelet activation; platelet aggregation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; pripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; lung ischaemia; thrombotic; cerebral ischaemia; thrombotic disorder; lung ischaemia; thrombosis; cerebral artery thrombosis; intracardiac thrombosis; peripheral artery thrombosis; peripheral artery thrombosis; peripheral artery thrombosis; peripheral artery thrombosis; carely sembolism; transient ischaemic attack; thrombos formation; occlusion; stenosis; restenosis; antianginal; cardiant;
                                                                                        GTACCTACATTCTCTCCCTCCTTCTGCAAGGCTATCATTTCACAGCTGATTCCTGGGAGC
                                                                                                                                                     ACATCCATTTCATTGGCAAGATCCAGGGCAGCGACGCCGGCTGGACTTTGGGCTACATGC
                                                              AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTGGGAGG
                                                                                AGATAAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTTCTG
                                                                                                                                                               ACATCCATTTCATTGGCAAGATCCAGGCAGCGACGACGCCGGCTGGACTTTGGGCTACATGC
                                                                                                                                                                                                   cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant.
coronary ischaemia; vascular occlusion; ss.
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/product= "Soluble CD39
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67. .1599
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(CORR ) CORNELL RES FOUND INC.
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The present cDNA sequence encodes soluble CD39 having apyrase activity.

This was derived from a cDNA library prepared from a human B cell line
referred to as MP-1. Soluble CD39 retains the capacity of wildtype CD39

to metabolise ATP and ADP at physiologically relevant concentrations as
well as the ability to block and reverse ADP-induced platelet activation

c and recruitment including platelet aggregation. This is used in the

creatment of unstable angina, myocardial infarction, stroke, coronary

c artery disease or injury, atherosclerosis, peripheral vascular occlusion,

preclampsia, embolism, platelet-associated ischaemic disorder including

cung ischaemia, ocronary ischaemia and cerebral ischaemia, a thrombotic

disorder including coronary attery thrombosis, cerebral artery

thrombosis, intracardiac thrombosis, peripheral artery thrombosis, thrombosis, coagulopathy, deep venous thrombosis, (DVT),

pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also

useful for preventing thrombus formation or reformation, occlusion,

c reocclusion, stenosis or restenosis of blood vessels or stroke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 GTTCAACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGCGG 100
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Inhibiting platelet activation and recruitment, useful for treating a mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTCTTCTCCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAG
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                                                                                                                                                                                                                                                                                                    The present invention relates to a method of treating cardiovascular disease in a subject, comprising administering an IL-17, IL-18, 4-1BB CD30 or OX40 antagonist. The IL-17, IL-18, 4-1BB, CD30 or OX40 antagonists are useful for treating cardiovascular disorders, e.g. (chronic immune) myocarditis, congestive heart failure, aneurysms, angina, embolism, restanosis, ischaemia or thrombocytopenic purpura, present sequence is a coding sequence used in the exemplification of invention.
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                                                                                                                                                                                                                Use of IL-17, IL-18, 4-1BB, CD30 or OX40 antagonists, for treating a cardiovascular disease, e.g. chronic immune myocarditis, congestive failure, aneurysm, angina, embolism, restenosis, ischemia or thrombocytopenic purpura.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1599;
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                                                                                                                                                                                                                                                                               Disclosure; Page 130-132; 135pp; English
                                                                                     28-AUG-2002; 2002US-0406418P. 12-AUG-2003; 2003US-0494457P.
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P-PSDB; ADL24295.
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                                                                       ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAGGACATTCAGGTTGCAAGTAATG
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                                                                                                                                                                           TTACAAGACCCCCTGCACCACCAAGATTTGAGATGACTCTTCCATTCCAGCAGTTTGAAA
                       CTCTGCAATTTCGCCTCTATGGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGCT
                                                                                                            AAATTCTCAGGGACCCATGCTTTCATCCTGGATATAAGAAGGTAGTGAACGTAAGTGACC
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Increasing or decreasing drug resistance in target bacteria, yeast, plant or mammalian cells comprises altering ATP gradient across biological membrane of target cell.
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                                                                                                                                                                                                                                                                                             The present invention relates to a method for increasing or decreasing drug resistance in target bacteria, yeast, plant or mammalian cells by altering the ATP gradient across the biological membrane of the target cell. The method is useful for modulating drug resistance of cells. It inseful for increasing the sensitivity of cells to chemotheraputic and antibiotic agents and increasing resistance to herbicides. The present sequence is human ATP diphosphohydrolase coding sequence. This sequence encodes was used in the present invention to modulate drug resistance. Note: The present sequence is not shown in the specification, but is referred to via its GenBank accession number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAG
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                                                                                                                                                         Lloyd
                                                                                                                                                       SJ,
                                                                                                                                                          Roux
                                                                                                                                                                                                                                                                        Claim 14; Page; 85pp; English.
                                                                     2000WO-US005315
                                                                                                  99US-00261825
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                                                                                                                            (TEXA ) UNIV TEXAS
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TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTGGGG
                                                                                                     ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAGGACATTCAGGTTGCAAGTAATG
                            GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATG
                                           GAGCCTCTACACACAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATG
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Disclosure; SEQ ID NO 1; 82pp; English
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Matches 1321; Conservative
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P-PSDB; ADJ57262.
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                            GAGCCTCTACACAAGTCACTTTTGTACCCAAAACCAGACTATCGAGTCCCCAGATAATG
                                                              CTCTGCAATTTCGCCTCTATGGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGCT
         GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATG
                                                                                      ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAGGACATTCAGGTTGCAAGTAATG
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The invention relates to a conjugate (I) comprising an enzyme and a biodegradable polymer, where (i) enzymatic activity of the enzyme is conjudeate to that of the enzyme in the absence of the blodegradable conjumer, or (ii) the half life of the enzyme is longer than that of the enzyme is longer than that of the caryme in the absence of the polymer. The enzyme is longer than that of the enzyme in the absence of the polymer. The enzyme is a multimeric, soluble and/or extracellular enzyme, preferably an apyrase, especially a soluble form of CD39 and catalyzes or preferably an apyrase, especially a soluble form of CD39 and catalyzes or preferably enzymed of extracellular nucleotides or abnormal levels of extracellular nucleotides or abnormal levels of extracellular nucleotides or abnormal levels of graft transplant. (I) is also used for treating coronary artery disease or injury following myccardial infarction, unstable angina, atherosclerosis, pre-eclampsia, embolism, coronary and thrombosis and coadulopathies associated with exposure to disorders, and thrombosis and coadulopathies associated with angioplasty, carotid endarterectomy, anastomosis of vascular grafts and chronic cardiovascular devices. The present sequence represents a DNA encoding a human CD39 polypeptide.
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                                                                                                                                                                                                                                                                                                                                                 New enzyme polymer conjugate used for treating abnormal levels of extracellular nucleotides or platelet aggregation, graft transplant, cardiovascular disease, cancer and sepsis.
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99.8%; Pred. No. 0;
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The bovine aorta (AAW04335 to AAW04318 and AAW04340) and porcine pancreatic (AAW04339) ATPDases have been partially sequenced. The agequences have been found to be highly homologous to a human lymphoid cell activation antigen designated CD39 (Maliazenski et at. (1994). J. Immunol.: 3574-3583). The complete sequences of the ATPDases types I and II have not been obtained yet. Assuming that the CD39 gene product is an ATPDase type II, the use of CD39 in the reduction of platelet aggregation and of thrombogenicity may be contemplated, as well as a process of making ATPDases using the CD39 sequence (AAT38516)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAG
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                                                                                                                                                                                                                           ATP diphosphohydrolase, ATPDase, bovine aorta; pig pancreas, apyrase; CD39; lymphoid cell activation antigen; enzyme; platelet aggregation; thrombogenicity; anti-haemostatic; ss.
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99.8%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                               Human lymphoid cell activation antigen CD39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Non-human transgenic or somatic recombinant mammals, whose cells contain a heterologous DNA encoding a polypeptide (especially human CD39 protein) having ATP-diphosphohydrolase activity under cellular activating conditions is claimed. In particular the animal is a pig and its cells (or tissues or organs) can be used for transplantation. DNA coding for human CD39 is also useful for genetically modifying a mammalian cell to render it less susceptible to an inflammatory or immunological stimulus and platelet aggregation. The modified cells can be used to prevent or alleviate a thrombotic condition. The present sequence encodes human CD39 protein and was disclosed in J.Immunol. 153 (8) (1994) 3574-3584
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/note= "CD39 protein has ATP diphosphohydrolase activity"
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                                                                                                                                                                                                                                                                            donor;
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The invention relates to a composition comprising a plurality of CDNAB Cordetecting the altered expression of genes in an immunological cresponse. The invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, comprising obtaining nucleic acids from a sample, contacting the nucleic acids of the sample with an array comprising the plurality of cDNAB under conditions to form one or more hybridisation complexes and comparing the levels of the detected hybridisation complexes with the level of hybridisation complexes with the level of hybridisation complexes with the level of hybridisation complexes correlates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and condition a plurality of polynucleotide probes. The CDNAB are useful as hybridisable array elements in a microarray for monitoring the expression of target polynucleotides. The microarray can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A composition comprising a plurality of CDNAs, useful for detecting altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma or osteoarthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, gene; 88; immunological response; immunopathological condition; Crohn's disease; asthma; ulcerative colitis; Myereosinophilia; irritable bowel syndrome; osteoarthritis; rheumatoid arthritis; actte monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer; osteopathic; antiarthritic; antirheumatic; cytostatic.
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the diagnosis of an immunopathology, such as Crohn's disease, asthma, ulcerative colitis, hypereosinophilia, irritable bowel syndrome, osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in identifying agents for the treatment of the diseases. The microarray may also be used in drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. The composition may also be used in purification of a subpopulation of mRNAs, cDNAs or genomic fragments. This sequence represents a human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly
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The invention relates to a novel pharmaceutical composition active on angiogenesis comprising an endothelial cell nucleic acid whose expression is induced by an angiogenic factor and inhibited by an angiostatic agent or its complement or fragment, a polypeptide sequence encoded by the nucleic acid or its fragment, a molecule capable of inhibiting expression of the nucleic acid or a molecule which binds to the polypeptide sequence. The invention is used to diagnose, prognose or treat an angiogenic disorder in a mammal, particularly a human. The disorder is particularly tumor vascularization, a retinopathy, rheumatoid arthritis, crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis, endometriosis associated with neovascularization, restenosis due to angiopatsy, overproduction of tissue due to cicatrisation, a peripheral vascular disease, hypertension, vascular inflammation, Raynaud disease, aneurism, arterial restenosis, thrombophlebitis, ischemia, angina, macular disease, thin farction, chronic heart disease, cardiac congestion or macular degeneration due to age or osteoporosis. This sequence
or polypeptide differentially expressed in angiogenesis.
                                                     Claim 2; SEQ ID NO 290; 424pp; French
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Sequence 1818 BP; 494 A; 418 C; 433 G; 473 T; 0 U; 0 Other;

ö 473 520 580 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATG 640 174 GGTTGACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGGATTGTGCTGGATGCCG 233 GITCITCICACACAGITIAIACAICIAIAAGIGGCCAGCAGAAAAGGAGAATGACACAG 160 GTTCTTCTCACACATTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACA 293 GCGTGGTGCATCAAGTAGAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC 220 GCGTGGTGCATCAAGTAGAAGAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC 353 AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGGGAAGTGA 280 TICCAAGGICCCAGCACCAAGAGACACCCGITITACCIGGGAGCCACGGCAGGCAIGCGGT 340 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGAGCC 400 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGAAGGTG 460 reaccaactaccecrireactrecaggereceaggareatracresecaagaggaggre 593 653 rcascarastroccarardaaaccaaraarcassaaaccrrrssascrrrssaccrrssss 713 773 CTCTGCAATTTCGCCTCTATGGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGCT 700 833 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATG CTCTGCAATTTCGCCTCTATGGCAAGGACTACAATGTCTACAACAATGTCTTGTGCT TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG GTTCAACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGCGG Gaps Length 1818; ö 3; Indels DB 12; Score 1319.2; I Pred. No. 0; 0; Mismatches 96.6%; ilarity 99.8%; Conservative Query Match Best Local Similarity Matches 1321; Conserv 234 161 221 414 641 41 101 294 354 281 341 474 401 534 461 594 521 654 581 셤 ઠે ద 셤 8 6 ò පු ò g ઠે g ò g ઠે g 셤 ò õ ò

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Genoscope.

Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invirrogen.

Location/Qualifiers
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25-normalized
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BP434894
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AGENCOURT
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AL572575
602926181
BP170295
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished
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AU121657
                                           BP141657
BP141351
                                                                                        BP171611
                                BP464335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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AL552087
BX402315
BP1652315
BP141657
BP141351
BP141351
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BP141351
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BP434198
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BP635137
AVI21657
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                                                                                                                                                                                                                                                                                                       1760 bp mRNA linear full-length cDNA clone CS0DI017YB13 of Placenta Cot of Memo sapiens (human).
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Pred. No. 3.2e-303;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/plasmid="pCMVSPORT_6"
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BQ958400
CA328573
AU121657
CD652289
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/db_xref="taxon:9606"
/clone="CSOCAP003YX21"
/tissue_type="THYMUS"
/clone lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and scoon the Not I and scoon sites of the pCMVSPORT 6 vector. Library was not normalized."
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           GTACCTACATTCTCTCCCTCCTTCTGCAAGGCTATCATTTCACAGTGATTCCTGGGAGC
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This sequence belongs to sequence cluster 5524.f

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0CAP003AF11QP1&c=5524.f.

Location/Qualifiers
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/organism="Homo sapiens"
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BX436692 Homo sapiens THYMUS Hc
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 2410)
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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Please visit our web site for further details.
URL:http://gancome.gsc.riken.jp/
URL:http://fancom.gsc.riken.jp/.
Location/Qualifiers
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                                              Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA
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High-efficiency full-length CDNA
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                                                                                 cDNA library'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                     /note="unnamed protein product; ectonucleoside triphosphate diphosphohydrolase 1 (MGD|MGT:102805, GB|NM 009848, evidence: BLASTN, 100%, match=2284) putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                 enriched mouse
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 863; DB 3; Length 2410;
Pred. No. 1.1e-243;
0; Mismatches 255; Indels 1
    xref="FANTOM_DB:4921511C05"
xref="taxon:10090"
                                                                 /tissue_type="testis"
/clone_lib="RIKEN full-length
                                   clone="4921511C05"
                                                                                             /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                              63.2%;
                                                     /sex="male"
                                                                                                                   .1645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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ENVKYGI VLDAGSSHTNLYI YKWPAEKENDTGVVQQLEECQVKGPGI SKYAQÄTDEI G
YVLAEKWELSTBLI PTSKHYOPVYLAGATGARILARNESSGABDVLAANSTSLKSYP
PDFQGAKI I TGQEEGAYGWI TI NYLLGKFTOGGSWLSLI SDSQKQETFGALDLGGGAST
QI TFVPQNSTI ESPENSLQFRLYGEDYTVYTHSPLCYGKDQALWQKLAKDI QVSSGGV
                                                                                                                                                                                                                                                              LKDPCFNPGYEKVVNVSELYGTPCTKRFEKKLPPDQFRIQGTGDYEQCHQSILELFNN
SEPCYSQCAFRGVFLPPLHGSFGAFSPAFYVNDFKKVAKVSIYGQERMTEITKNRCS
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/db_xref="GI:26326591"
/translation="MEDIKDSKVKRFCSKNILIILGFTSILAVIALIAVGLTQNKPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        324 GTGCAGCAGTTAGAGGAATGCCAAGTGAAAGGTCCTGGAATCTCAAAATATGCTCAGAAA 383
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     GB|NM_009848, evidence: BLASTN, 100%, match=2284)
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79.8%; Pred. No. 1.3e-243;
ive 0; Mismatches 255;
                                                                                                                                                                                                                                                                                                                                                                                                                         /note="putative"
4198
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                            Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watshikagi,K., Yonacada,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Shazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer 20530913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,70 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4198)
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'clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKRN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehitro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-922,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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triphosphate diphosphohydrolase 1 (MGD|MGI:102805,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gec.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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db_xref="taxon:10090"
clone="5330437E10"
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/strain="C57BL/6J"
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                                                                                                                       /clone="CSODIO73YD08"
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and BCOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
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organism="Homo
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was ptimed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSDRT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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to sapiens cDNA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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BX371889 Homo sapiens PLACENTA COT 25-NORWALIZED Homo
clone CSODI073YD08 3-PRIME, mRNA sequence.
BX371889.2 GI:46831287
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Onpublished (2001)
On May 8, 2003 this sequence version replaced
Contact: Genoscope
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/ DECOLET 100="ISKYAQKTDEIGAYLAECMELSTELIPTSKHQTPVYLGATAGM

/ Lanala 14 too="ISKYAQKTDEIGAYLAECMELSTELIPTSKHQTPVYLGATAGM

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SPLCYGKDQALWQKLAKDIQVSSGGVLKDPCFNPGYEKVVNVSELYGTPCTKRFEKKL

DFFKYVAKNSVISQENTEITKNFCSKSWEETKTSYPSVKFKYLSEYCFSGAYILSLL

QGYNFTGSSRRQIHFKKINGSNAGWTLGYMLNTNNIPAEQPLSPPLPHSTYIGLMV

LESLLVAVALTGLFIYSKPSYFWKEAV"
     Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (SCC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gec.riken.jp, WIR.:http://genome.gec.riken.jp, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue type="skin"
/clone_lib="RikEN full-length enriched mouse cDNA library"
/dev_atage="10 days neonate"
<1. .1265
                                                                                                                                                                                                  cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKBN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 504 TCAGAAAACAAGGTGGTTCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGG 563
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triphosphate diphosphohydrolase 1 (MGD|MGI:102805,
GB|Ny 009848, evidence: BLASTN, 100%, match=2284)
putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3563;
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                                                                                                                                                                                                                                                                                                           prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gec.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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/db xref="taxon:10090"
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/mol_type="mRNA"
/strain="C57BL/6J"
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/note="putative"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Lot 60,770 full-length cDNAs

Lot 60,770 full-length cDNAs

Lot 60,263-573 (2002)

E (bases I to 3563)

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                                                                                                                                                                                                                                                                           AK028625

Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732419M16 product:ectonucleoside triphosphate diphosphohydrolase 1, full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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81 ACTCTTCCATTCCAGCAGTTTGAAATCCAGGGTA-TGGAAACTATCAACAAT-CCATCAA
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Functional annotation of a full-length mouse cDNA collection
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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/clone="CS0DI073YD08"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1014)

359 CGCTTTGGATCTCGGCGGAGCCTCCACACATCACCTTCGTGCCCCAAAACAGCACTAT
                                                                                        ACATAGCTICTICTGCTATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAGGACT
                                                                                                                              599 rereaareraacreaecrerareceaerecereceaaaaaarrecaaaadaaeeraee
                                                                                                                                                                                                                                           ATTCCAGCAGTTTGAAATCCAGGGTATTGGAAACTATCAACAATGCCATCAAAGCATCCT
                                                                                                                                                                                                                                                         924 GGAGCTCTTCAACACCCAGTTACTGCCCTTACTCCCAGTGTGCCTTCAATGGGATTTTCTT
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                                AGCTTTGGACCTTGGGGGGAGCCTCTACACAGTCACTTTTGTACCCCAAAACCAGACTAT
                                                                         CGAGTCCCCAGATAATGCTCTGCAATTTCGCCTCTATGGCAAGGACTACAATGTCTACAC
                                                                                                                                                                              539 rcaddrircaadrogrocorcorraaddaccardcriraacccaddaracdaaaddr
                                                                                                                                                           TCAGGTTGCAAGTAATGAAATTCTCAGGGACCCATGCTTTCATCCTGGATATAAGAAGGT
                                                                                                                                                                                                   804 AGTGAACGTAAGTGACCTTTACAAGACCCCCTGCAACAAGAGATTTGAGATGACTCTTCC
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clone CSODI073YD08 5-PRIME, mRNA sequence.
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Pull-length cDNA libraries and normalization
Li Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31274964.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a Noti-oligo(dT) primer. Five prime end enriched, double-errand cDNA was digested with Not I and cloned into the Not I and Ecor V sites of the pCWNSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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604 520 664 580 724 640 784 700 844 758 904

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AL552123 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA Clone CSODIO59YC11 5-PRIME, mRNA sequence.
AL552123
AL552123.3 GI:45856912
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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B. (Dabses I to 1066).

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLANL2714 row: c column: 20

High quality sequence stor: 2

High quality sequence stor: 64.
                                                                                                                                                                                                                                                                                                                                                                                                        BM906668 1066 bp mRNA linear EST 12-MAR-2002 AGENCOURT_6621802 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:57246195', mRNA Fequence.
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//olone lib="Organ: ovary" (pool of 3); Vector: pCMV-SPORT6;
Site 1: ECORV (destroyed); Site 2: Not1; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(ECORV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."
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                                                                                                                   ATGGGAAGGATCAGGCACTCTGGCAGAACTGGCCAAGGACATTCAGGTTGCAAGTAATG
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Pred. No. 1.6e-203;
0; Mismatches 45; Indels 11; Gaps
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/organism="Homo sapiens"
/ol_types=mRNN"
/db_xref="taxon:9606"
/clone="TMAGE:5724619"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM906668.1 GI:19357047
                                                                                                                                                                                                                       761 AAATTCTCAGGGACC 775
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Homo sapiens
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998

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Contact: Genoscope Control of Sequences of Service Ser
                                                                                                                                                                                                                                                                                                                                     BX402316 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI017YB13 5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 1025)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30610946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-Oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
751 ATGGGAAGGATCAGGCACTCTGGCAGAACTGGCCAAGGACATTCAGGGTGCAAGTAATG
                                                     AAATTCTCAGGGACCCATGCTTTCATCCTGGATATAAGAAGGTAGTGAACGTAAGTGACC
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                                                                                AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGGGAAGTGA
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                                                                                                                                                            851
                                                                                                                                                                                         821 TTTACAAGACCCCTGCACCAAGAGATTTGA
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/db_xref="taxon:9606"
/clone="CS0D1017YB13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens (human)
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  Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
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/clone="Ib="PLACENTA COT 25-NORWALIZED"
/clone=Tib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/clone=Tist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                      5524.f
For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODI059AB06QPl&c=5524.f.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.8%; Score 720.6; DB 1; Length 897; 94.3%; Pred. No. 1.2e-201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
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Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 952)
1 (Aruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                  308 GCGTGGTGCATCAAGTAGAAGAATGCMGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC
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Pred. No. 8.4e-195;
5; Mismatches 5;
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1. (base 1 to 1023)

2. Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

3. Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

4. Unpublished (2001)

5. Ton Feb 15, 2001 this sequence version replaced gi:31269551.

6. Contact: Genoscope

Genoscope - Centre National de Sequencage

7. Toe Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE

8. Email: seqref@genoscope.cns.fr. Web: : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALS47722
ALS47722
ALS47722 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA Clone CS0DI017YB13 5-PRIME, mRNA sequence.
ALS47722
ALS47722.3 GI:45748162
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/tissue rype="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
                                                                                                                                                                                                                                                                                                  TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGTG
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                                            428 TICCAAGGICCCAGCACCAAGAGACACCCGTITACCIGGGAGCCACGGCAGGCAIGCGGI
                                                                             TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                    For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODI017CA07QP1&c=5524.f. Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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CTGGGCAAATTCAGTCAGAAAACAAGGTGGTTCAGCATAGTCCCATATGAAACCAATAAT
                                    1341 CACACCTCTCTCCCACTCCAC 1361
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                                                                      682 cacaccrercrrccacrccac
                                                                                                                                                                                                                               BM925184.1 GI:19375563
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Homo sapiens
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5', mRNA Bequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
Contact: Genoscope Genoral de Sequencage Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr lst strand cDNA was primed with a NotI-oligo(dI) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATCCCAGCTGAGCAACCATTGTC 1340
                                                                                                                                                                            For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAG036ZD06_CS03404_1&c=5524.f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTGCCACCACTCCAGGGGGATTTTGGGGCATTTTTCAGCTTTTTACTTTGTGATGAAGTT 1040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTGCCACCACTCCAGGGGGTTTTTGGGCATTTTTCAGCTTTTTACTTTGTGAAGTT 382
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                                                                                                                                                                                                                                                                                                                                /tissue type="PIACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.1%; Score 656.8; DB 5; Length 952; 98.7%; Pred. No. 1e-182; ive 0; Mismatches 8; Indels 1
                                                                                                                                                                                                                                                      l. .ysz
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI073YD08"
                                                                                                                                                                                                                               Location/Qualifiers
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/lab host="DH108"
/lab host="DH108"
/clone lib="NHH MGC 122"
/clone lib="NHH MGC 122"
/note="Organ: pooled lung and spleen; Vector: pCWV-SPORT6;
Site_l: Not1; Site_2: EccRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20.22 week male spleens. Library is oligo-dr
primed and directionally cloned (EccRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                      1061 bp mRNA linear EST 12-MAR-2002
.6627603 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5762493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 GGTTGACCCAGAACAAGCATTGCCAGAAACGTTAAGGATGGAAAGTGAAGAGTTGGCA 231
623 CTGGACTTTGGGCTACATGCTGAACCCTGACCACATGATCCCAGCTGAGCAACCATTGT- 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (basea 1 to 1061)
NIH-MGC http://mgc.noi.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
n column: 22
High quality sequence start: 4
High quality sequence stop: 669.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5762493"
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/mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:4309839"
/tlssue type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone=lib="mNHI MGC 48"
/note="Organ: B-cells, Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTACCCCAAAACCAGACTATGGAGTCCCCAGATAATGCTCTGCAATTTCGCCTCTATGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          477 GAGATGAAAAAGTTCTGTGCTCAGCCTTGGGAGGAGATAAAAACATCTTACGCTGGA
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                                                                                                                                                                                                                                                                                                                                                      Length 808;
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                                                                                                                                                                                                                                                                                                                                                    Score 645.2; DB 2;
Pred. No. 2.6e-179;
0; Mismatches 3;
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E. (Dasses I to 808)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1183 row n column: 16

High quality sequence stop; 758.
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  CTGGGCAAATTCAGTCAGAAACAAGGTGGTTCAGCATAGTCCCATATGAAACCAATAAT
                                                               CAGGAAACCTTTGGAGCTTTGGACCTTGGGGGAGCCTCTACACACAAGTCACTTTTGTACCC
                                                                                                                                              GAGATGACTCTTCCATTCCAGCAGTTTGAAATCCCAGGTATTGGAAACTATCAACATGC
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                                                                                                                         CAAAACCAGACTATCGAGTCCCCAGATAATGCTCTGCAATTTCGCCTCTATGGCAAGGAC
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                                          CAGGAAACCTTTGGAGCTTTGGACCTTGGGGGAGCCTCTACACAAGTCACTTTTGTACCC
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Homo sapiens
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                                                                                                                                                                                                                                                               University of Washington
Box 358070, Seattle, WA 98195-8070, USA
Box 358070, Seattle, WA 98195-8070, USA
Box 326 732 6155
Email: ted@locke.hs.washington.edu
Similar to GenBank entry S73813 S73813 CD39=lymphoid cell
activation antigen [human, B lymhpoblastoid cell line, MP-1, mRNA, 1818 ncl. 4/1995
Plate: MMSP0076 row: A column: 03.
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                                                                                       Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca. I (bases 1 to 673)
Ratze, M.G., Bumgarner, R., Korth, M., Feldman, R., Amjadi, M. and Holzman, T.
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     MMSP0076_A03 MMSP Macaca mulatta cDNA, mRNA sequence.
                                                                                                                                                                                                 Expressed sequence tags from Rhesus macaque spleen Unpublished (2002)
Contact: Holzman T
                                                                                                                                                                                                                                                                                                                                                                                                   ISP0076 row: A column: 03 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Macaca mulatta"
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/dev_gtage="adult"
/clone_lib="MMSP"
/note="Organ: spleen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9544"
/sex="male"
                                                             Macaca mulatta (rhesus monkey)
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        1191

        Db
        481 TCTTACGCTGGAGTAAAGGAGAAGTACCTGGAGATACCTGGTACCTACATT
        154

        CTCTCCTGGAGGAAAGGAAGTACCTGGAGAATACCTGGGAGCACATT
        154

        Db
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        150

        Qy
        1251 CATTGGCAAGATCCAGGCTATTTTCACAGCTGATTCCTGGAGCACATCCATTT
        600

        Qy
        1251 CATTGGCAAGATCCAGGCAGCCGCGCTGGGAGTTTTGGGCTACATGCTGAACCTGA
        1309

        Db
        601 CATTGGCAAGATCCAGGCAGCGCGGCTGGGGACTTTGGGCTACATGCTGAACCTGA
        600

        Qy
        1310 CCAACATGATCCC
        1322

        Qy
        1310 CCAACATGATCCC
        132

        CCAACATGATCCC
        673
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Search completed: September 21, 2005, 23:22:02 Job time : 4882.93 secs

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AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGGAAGGGAAGGA
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Sequence 13, Appl
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Sequence 17392, A
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Sequence 190884,
Sequence 18084, A
Sequence 15639, A
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; OTHER INFORMATION: Description of Unknown Organism: unknown
US-08-930-921-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indela
                                                                                                                                                                                                                                                                                                                                    APPLICANT: BEAUDOIN, Adrien R.
APPLICANT: SEVIGNY, Jean
TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF ITILE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEIR OF INVENTION: TECHNOLOGY
TITLE OF INVENTION: TECHNOLOGY
FILE REPERENCE: ATP-DIPHOSPHOHYDROLASES-BEAUDOIN
CURRENT APPLICATION NUMBER: US/08/930,921B
CURRENT FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: PCT/CA96/00223
EARLIER FILING DATE: 1996-04-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
LENGTH 1818
US-09-949-016-21380
US-09-129-112-8
US-09-129-112-8
US-09-129-112-18
US-09-129-112-18
US-09-350-808-58A-6
US-09-370-265-6
US-09-370-265-6
US-09-370-265-6
US-09-949-016-12583
US-09-949-016-1395
US-09-949-016-13804
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US-09-608-285A-1
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99.8%; Pred. No. 0;
ive 0; Mismatches
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; Sequence 2, Application US/08930921B
; Patent No. 6287837
; GENERAL INFORMATION:
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Best Local Similarity 99.8
Matches 1321, Conservative
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                                                            GENERAL INFORMATION:
APPLICANT: Cocke, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: OFFICE OF STAND STA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WARD PERFECT 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.6%; Score 1319.2;
99.8%; Pred. No. 0;
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                       Sequence 1475, Application US/09023655 Patent No. 6607879
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-00
TELECOMMUNICATION INFORMATION:
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1475:
SEQUENCE CHARACTERISTICS:
LENGTH: 1818 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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Best Local Similarity 99.8
Matches 1321; Conservative
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; LIBRARY: GENBANK
; CLONE: 9765255
US-09-023-655-1475
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                                                                                      TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGAGGAGGTG
                                                                                                                                                                                                    GAGCCTCTACACACAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATG
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Sequence 2, Application US/09781796C Patent No. 6800284 GENERAL INFORMATION:
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Best Local Similarity 99.8
Matches 1321; Conservative
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ORGANISM: Homo sapiens
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GENERAL INVENDATION

JAPPLICANT: BEAUDOIN, Adrien R.

APPLICANT: BEAUDOIN, Jean

APPLICANT: BEVIGNY, Jean

APPLICANT: BACH, Fritz H.

APPLICANT: BACH, Fritz H.

APPLICANT: ROBSON, Simon

TITLE OF INVENTION: THEREOF AND PROCESS OF PURIFICATION

TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT

TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT

TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT

TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT

TITLE OF INVENTION WINBER: U8/99/204

PRIOR PAPLICATION NUMBER: U8/419,204

PRIOR PAPLICATION NUMBER: CA96/00223

PRIOR PAPLICATION NUMBER: CA96/00223

PRIOR PAPLICATION NUMBER: 08/930,921

PRIOR PAPLICATION NUMBER: 08/930,921

PRIOR APPLICATION NUMBER: 08/930,921

PRIOR PAPLING DATE: 1998-02-01

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PALEALIN Ver. 2.1

SEG ID NO 2

FONCELLING DATE: PALEALIN VER. 2.1 ô 353 773 233 GTTCTTCTCACACAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAG 160 293 220 280 413 340 473 400 533 460 593 520 653 580 713 640 234 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAG GTTCAACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGCGG GGTTGACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGCGG 354 AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGGAAAGTGA TCAGCAACTACCCCTTTGACTTCCAGGTGCCAGGATCATTACTGGCCAAGAGGAAGGTG TCAGCATAGTCCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGGG GCGTGGTGCATCAAGTAGAAGAATGCAGGGTTAAAAGGTCCTGGAATCTCAAAATTTGTTC 294 GCGTGGTGCATCAAGTAGAAGAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGAAGGTG TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTTGGACCTTGGGG GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATG AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGGGAAGTGA TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGAGCCC Gaps ö DB 4; Length 1818; Indels ., m 96.6%; Score 1319.2; 99.8%; Pred. No. 0; ive 0; Mismatches 714 요 ઠે

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Pred. No. 2.3e-144;
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                                                     Query Match 33.9%;
Best Local Similarity 99.4%;
Matches 465; Conservative
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2106
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ORGANISM: Human
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TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (83)..(1669)
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APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Brian Paul
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO;
TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
TILE REFERENCE: 9598-066; CURRENT APPLICATION NUMBER: US/09/240,639; CURRENT FILING DATE: 1998-01-29; NUMBER OF SEQ ID NOS: 29; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 3; SEQ ID NO 3 ဥ CATGCTGAACCTGACCAACATGATCCCAGCTGAGCAACCATTG 1470 CATGCTCAGCCTGACCAACCAGATCCCAGCTGAAAGCCCTCTG Query Match
21.3%; Score 291; DB 3;
Best Local Similarity 54.3%; Pred. No. 3.6e-86;
Matches 707; Conservative 0; Mismatches 575 528 8 8

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                      TYPE: DNA
ORGANISM: Homo Sapiens
PEATURE:
NAME/KEY: CDS
LOCATION: (83)...(1669)
OTHER INFORMATION:
      2797
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APPLICANT: Chadwick, Anna Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS
FILE REFERENCE: 28110/36120E
CURRENT APPLICATION NUMBER: US/09/908,510A
CURRENT APPLICATION NUMBER: 09/240,639
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 3
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Patent No. 6759214
GENERAL INFORMATION:
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NUMBER OF SEQ 1D NOS: 32
SOFTWARE: Patentin version 3.1
SEQ 1D NO 3
LENGTH: 2797
TYPE: DNA
PRATURE: FEATURE:
NAME/KEY: CDS
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; OTHER INFORMATION:
US-10-107-576-3
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                                                                                       APPLICANT: Frischauf, Anna-Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
FILE REPERENCE: 9598-066
CURRENT APPLICATION NUMBER: US/10/107,660
CURRENT FILING DATE: 2002-03-27
PRIOR FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                      21.3%; Score 291; DB 4; Length 2797; 54.3%; Pred. No. 3.6e-86; ive 0; Mismatches 575; Indels 2
                               ; Sequence 3, Application US/10107660; Patent No. 6780977; GENERAL INFORMATION:
                                                                              APPLICANT: Chadwick, Brian Paul APPLICANT: Frischauf, Anna-Mar.
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Matches 707; Conservative
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                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: (83)..(1669)
US-10-107-660-3
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GGATCAGGCACTCTGGCAGAAACTGGCCAAGGACATTCAGGTTGCAAGTAATGAAA---T 764
                                                                                                                                                   GAÁTGAGGCTGAGAAGATTCTGGCAATGCTCCTGCAGAATTCTCCTACCAAAAACCA
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                                                                                                                                                                                                                             TCTCAGGGACCCATGCTTTCATCCTGGATATAAGAAGGTAGTGAACGTAAGTGACCTTTA
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Sequence 3, Application US/10107576
Patent No. 678359
SEGREAL INFORMATION:
APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna Maria
TITLE OF INVENTION: METHODS AND COMPOSITION:
TITLE OF INVENTION: ACIDS
FILE REFERENCE: 28110/36120H
CURRENT APPLICATION NUMBER: US/10/107,576
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: 09/240,639
PRIOR FILING DATE: 1999-01-29
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APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Brian Paul
APPLICANT: Crischauf, Anna Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
FILE REFERENCE: 28110/361208
CURRENT APPLICATION NUMBER: US/09/905,7328
CURRENT APPLICATION NUMBER: 090240,639
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 32
SOFFWARE: Patentin version 3.1
   GCCCCAAATACACTTTGAAAAGAAGTGGGGAATAGCAGCATAGCCTGGTCTCTTGGCTA 1470
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                                                                                                                      TICTGGTACCTACATTCTCCCTCCTTCTGCAAGGCTATCATTTCACAGCTGATTCCTG
                                                                                                                                            CTCAGCCAACTACATCTACCACTTGTTTGTGAACGGTTACAAATTCACAGAGGAGACTTG
                                                                                                                                                                                        GGAGCACATCCATTCGATGGCAAGATCCAGGGCAGCGACGCCGGCTGGACTTTGGGCTA
                                                                          GGAGGAGATAAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTT
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Patent No. 6787328
GENERAL INFORMATION:
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ORGANISM: Homo Sapiens
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LOCATION: (83)..(1
COTHER INFORMATION:
US-09-905-732B-3
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                                                                                                 CAAGCAAGAGGTCCTCCCAGGACTGAAGTATGGTATTGTGCTGGATGCCGGGTCTTC
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                                    Gaps
                                    21;
     Length 2797;
 Score 291; DB 4; Length 27
Pred. No. 3.6e-86;
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FILE REFERENCE: UTSC:658US
CURRENT APPLICATION NUMBER: US/09/923,304
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 2797
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                             tch 21.3%; al Similarity 54.3%; 707; Conservative
                                                                                                               ; NAME/KEY: CDS
; LOCATION: (83)..(1672)
US-09-923-304-3
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Sequence 3, Application US/09923304

Patent No. 6797471

GENERAL INFORMATION:

APPLICANT: KATZ, RUTH

APPLICANT: JIANG, FENG

TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS

US-09-923-304-3

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CAGTCAAACCTTCAAATGTAGTGTGAAAGGCTCTGGAATCTCCAGCTATGGAAATAACCC 399
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Sequence 178, Application US/09949016

Batent No. 681239

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 178

LENGTH: 2797
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                AATCCAGGGTATTGGAAACTATCAACAATGCCATCAAAGCATCCTGGAGCTCTTCAACAC
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Pred. No. 3.6e-86;
0; Mismatches 575; Indels
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21.3%;
Best Local Similarity 54.3%;
Matches 707; Conservative
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                                                                 ATTTCGCCTCTATGGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGCTATGGGAA
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Sequence 13648, Application US/09949016
Fatent No. 681239
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
TITLE REPERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
FRIOR PILING DATE: 2000-10-03
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR PILING DATE: 2000-10-03
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR PILING DATE: 2000-10-03
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR SEQ ID NOS: 207012
SOFTWARE FEASTER FEASTER FOR Windows Version 4.0
SEQ ID NO 13448
LENGTH: 46885
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US-09-949-016-13848
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llarity 54.3%; Pred. No. 3.6e-86;
Conservative 0; Mismatches 575; Indels 2
                          1296 CATGCTGAACCTGACCAACATGATCCCAGCTGAGCAACCATTG 1338
1471 CATGCTCAGCCTGACCAACCAGATCCCAGCTGAAAGCCCTCTG 1513
                                                                                                                                                                                                                                   APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Brian Paul
TITLE OF INVENTION: METHODS AND COMPOSITIONS
TITLE OF INVENTION: ACIDS
FILE REFERENCE: 28110/36120C
CURRENT APPLICATION NUMBER: US/09/905,743B
CURRENT APPLICATION NUMBER: 09/240,639
PRIOR APPLICATION NUMBER: 09/240,639
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 2797
                                                                                                                                                                          ; Sequence 3, Application US/09905743B; Patent No. 6828423; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (83)..(1669)
COTHER INFORMATION:
US-09-905-743B-3
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Best Local Similarity
Matches 707; Conserv
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                                                                                                       0; Gaps
                                                                                Query Match
Best Local Similarity 98.9%; Pred. No. 2.8e-78;
Matches 272; Conservative 0; Mismatches 3; Indels 0;
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; TYPE: DNA; ORGANISM: Human; FEATURE:; NAME/KEY: misc_feature; LOCATION: (1)...(46885); OTHER INFORMATION: n = A,T,C or GUS-09-949-016-13848
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1: /cgn2 6/prodata/1/pubpna/US07 PUBCOMB.seq:*
2: /cgn2 6/prodata/1/pubpna/PCT NEW PUB.seq:*
4: /cgn2 6/prodata/1/pubpna/US06 NEW PUB.seq:*
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12: /cgn2 6/prodata/1/pubpna/US09 PUBCOMB.seq:*
11: /cgn2 6/prodata/1/pubpna/US09 NEW PUB.seq:*
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22: /cgn2 6/prodata/1/pubpna/US10A PUBCOMB.seq:*
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                               GenCore version
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 5, Appli Sequence 7, Appli Sequence 25, Appl Sequence 1, Appli Sequence 29, Appl Sequence 1475, Ap Description US-09-835-147-5 US-09-835-147-7 US-09-835-147-1 US-09-835-147-1 US-10-646-308-29 US-10-641-641-1475 US-10-934-998-290 SUMMARIES H <u>0</u>8 Match Length 1365 1437 1464 1599 1599 1818 100.0 100.0 97.3 96.6 96.6 96.6 Query Score 1365 1365 1328 1319.2 1319.2 1319.2 1064597 Result

Sequence 46, Appl Sequence 147, App Sequence 193, App Sequence 23052, A Sequence 23052, A Sequence 23, Appl Sequence 3, Appl Sequence 2, Appl Sequence 2, Appl Sequence 21, Appl Sequence 21, Appl Sequence 495, App Sequence 495, A	ivation and Recruitment
2 US-10-934-998-46 6 US-10-240-965-242 2 US-10-934-998-1937 0 US-10-934-998-1937 0 US-10-934-998-1937 0 US-10-934-998-1937 0 US-10-934-998-1937 2 US-10-1002-2136 0 US-10-1076-918-295 0 US-10-1076-918-295 0 US-10-1076-918-295 0 US-10-1076-918-495	ALIGNMENTS 35147  as R.  a of Platelet Act 13 5/09/835,147 50/104,585 50/107,466 50/149,010 70S99/22955
2.2 96.6 4 44 9 6 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	S-09-835-147-5 Sequence 5, Application US/09835 Sequence 5, Application US/09835 Batent No. US2002002277Al GENERAL INFORMATION: APPLICANT: Gayle III, Richard APPLICANT: Gayle III, Richard APPLICANT: Gayle III, Richard APPLICANT: Gampel, Steven D. TITLE OF INVENTION: Inhibitors FILE REFERENCE: 2879-US CURRENT APPLICATION NUMBER: US/CURRENT APPLICATION NUMBER: US/OPRIOR PRIOR PILING DATE: 1998-10-16 PRIOR FILING DATE: 1998-10-06 PRIOR FILING DATE: 1999-08-13 PRIOR FILING DATE: 1999-09-13 PRIOR FILING DATE: 1999-09-13 PRIOR FILING DATE: 1999-09-13 RIGHT APPLICATION NUMBER: DCT/US PRIOR FILING DATE: 1999-09-13 RIGHT APPLICATION NUMBER: DCT/US PRIOR FILING DATE: 1999-09-13 RIGHT APPLICATION NUMBER: DCT/US PRIOR FILING DATE: 1999-09-13 RUMBER OF SEQ ID NOS: 31 SOFTWARE: PATENTIN UMBER: PCT/US TYPE: DNA ORGANISM: ATTIFICIAL SEQUENCE FEATURE: OTHER INFORMATION: CORSTINCTO
C C C C C C C C C C C C C C C C C C C	RESULT 1 US-09-835-147; Sequence 5; Patent No.; GENERAL INF SAPPLICANT: APPLICANT: APPLI

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Sequence 7, Application US/09835147

Sequence 7, Application US/09835147

Setent No. US2002002077A1

GENERAL INFORMATION:

APPLICANT: Maliszewski, Charles R.

APPLICANT: Gayle III, Richard B.

APPLICANT: Gimel' Steven D.

TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE REFERENCE: 2879-US

CURRENT APPLICATION NUMBER: US 60/104,585

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1999-08-13

PRIOR APPLICATION NUMBER: US 60/149,010

PRIOR APPLICATION NUMBER: PCT/US99/22955

PRIOR APPLICATION NUMBER: PCT/US99/22955

PRIOR PLING DATE: 1999-08-13

NUMBER OF SEQ ID NOS: 31

SEQTIMARE PATENT OF SET 
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Best Local Similarity 100.
Matches 1365; Conservative
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; LOCATION: (1)..(1434)
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             ATCCAGGGCAGGCGGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATC
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                                                                                         Score 1328; DB 9; Length 1
Pred. No. 0;
0; Mismatches 21; Indels
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NAME/KEY: CDS
LOCATION: (1)...(1461)
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: construct of human CD39
US-09-835-147-25
                                                                                                                                                                       Sequence 215, Application US/09835147

Patent No. US2002002277A1

GENERAL INFORMATION:
APPLICANT: MAINESWERKI, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Gimpel, Virginia L.
APPLICANT: Gimpel, Stewn D.
TITLE OF INVENTION: Inhibitors of Platelet Act FILE REFERENCE: 2079-02.
FILE REFERENCE: 2079-035, 147
CURRENT FLING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR PRILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VET. 2.0
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Best Local Similarity 98.5%;
Matches 1334; Conservative (
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Sequence 1, Application US/09835147	Query Match         96.6%;         Score 1319.2;         DB 9;         Length 1599;           Best Local Similarity         99.8%;         Pred. No. 0;         3         Indels         0;         Gaps           Matches 1321;         Conservative         0;         Mismatches         3;         Indels         0;         Gaps           41         GTTCAACCCAGAACAAGACATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGGG         10         11 <td< th=""><th>  Db   173 GGTTGACCCAGAACAAAGGATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGCGG 232    </th><th>Qy         221 AGAAAGTAAATGAAATAGGCATTTACCTGACTGGTAGGAAAGAGTGA 280  </th><th>Qy         341 TGCTCAGGATGGAAAGTTGACGACACAGGGTTCTGGATGTGGTGGAGAGCC         400  </th><th>461 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAATTCAGTCAG</th><th>581 GAGCCTCTACACAAGTCACTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATG 581 GAGCCTCTACACAAGTCACTTTTGTACCCCCAAAACCAGACTATCGAGTCCCCAGATAATG 713 GAGCCTCTACACAAGTCACTTTTGTACCCCCAAAACCAGACTATCGAGTCCCCAGATAATG</th></td<>	Db   173 GGTTGACCCAGAACAAAGGATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGCGG 232	Qy         221 AGAAAGTAAATGAAATAGGCATTTACCTGACTGGTAGGAAAGAGTGA 280	Qy         341 TGCTCAGGATGGAAAGTTGACGACACAGGGTTCTGGATGTGGTGGAGAGCC         400	461 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAATTCAGTCAG	581 GAGCCTCTACACAAGTCACTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATG 581 GAGCCTCTACACAAGTCACTTTTGTACCCCCAAAACCAGACTATCGAGTCCCCAGATAATG 713 GAGCCTCTACACAAGTCACTTTTGTACCCCCAAAACCAGACTATCGAGTCCCCAGATAATG
10   TTTACCTGGGAGCCACGGCATGCGTTGCTCAGGATGGAAAGTTGAAGGTTGCAG 469     371   ACAGGTTCTGCATGTGGTGGAGAGCACTACCCCTTTGACTTCCAGGTG 430     470   ACAGGTTCTGCATGTGGAGAGAGCACTACTACTCCCTTTGACTTCCAGGTG 529     471   ACAGGTTCTGCATGTGGAGAGAGAGCTCAGCACTACTACTCCAGGTG 529     470   ACAGGTTCTGATGTGGAAGAGAGAGAGCTCAGCATACTACTCAGGTG 529     491   TGGGAAATTCAGTCAGAAAGGTGGTTCAGCATAGTACTATCAACTATCTGC 589     491   TGGGAAATTCAGTCAGAAACAGGTGGTTCAGCATAGTACTATCAACTATCTGC 589     491   TGGGAAATTCAGTCAGAAACAGGTGGTTCAGCATAGTACTATCAACTATTGTACCATATTGTACTGC 589     491   TGGGAAATTCAGTCAGAAACAGGTGGTTCAGCATAGTACTATCAACTATTGTACCATATTGTACTGC 590     492   TGGGCAAATTCAGTCAGAAACAGGTGGTTCAGCATAGTACTATTGTACCATTATTGTACCATATTGTACTGC 590     493   TGGGCAAATTCAGTCAGAAACAGGTGGTTCAGCATAGTACAATTTGTACTATTGTACTGC 590     494   TGGGCAAATTCAGTCAGAAACAGGTGGTTCAGCATATTTGTACTATTTTTTTT	791 GATATAAGAAGGTAGTGAACGTAAGTGACCTTTACAAGACCCCCTGCACCAAGAGATTTG	Db   950 AGATGACTCTTCCATTCCAGCACTTTGAAATCCAGGGTATTGGAAACTATCAACAATGCC 1009	1031 TGATGAAGTTTTTAAACTTGACATCAGAGAAAGTCTCTCAGGAAA 1130 TGATGAAGTTTTTAAACTTGACATCAGAGAAAGTCTCTCAGGAAA 1130 TGAAAAAGTTTTTAAACTTGACATCAGAGAGAGAGAGAAACTTCTCTCAGCAAA 1091 TGAAAAAGTTCTGTGCTCAGCCTTGGGAGAGAGATAAAAAACTTCTT 1190 TGAAAAAGTTCTGTGCTCAGCCTTGGGAGGAGAAAAAAAA	Qy         1151 AGAAGTACCTGGGTTTTCTGGTACCTACATTCTCTCCCTCC	1271 GCGACGCCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATCCCAGGTGAGC  1370 GCGACGCCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATCCCAGGTGAGC  1331 AACCATTGTCCACACCTCTCCCCACTCCACAACATGATCCCAGGTGAGC  1331 AACCATTGTCCACACCTTCTCCCACTCCACAAA 1365	1430 AACCAIIGICCACACCICICLCCACICCACICAACCIAA 14 SULF 4 -09-835-147-1

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llarity 99.8%; Pred. No. 0;
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                                                                                Similarity
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; NAME/KEY: CDS
; LOCATION: (67).
US-10-646-308-29
TYPE: DNA
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Publication No. US20040136992A1

GENERAL INFORMATION:

APPLICANT: BURING.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE

TITLE OF INVENTION: LOAD-12

CURRENT APPLICATION NUMBER: US/10/646,308

CURRENT FILING DATE: 2003-08-21

PRIOR FILING DATE: 2003-08-28

NUMBER OF SEQ ID NOS: 36

SEQ ID NOS: 36

LENGTH: 1599
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Pred. No. 0;
0; Mismatches
               LIBEARY: GENBANK
CLONE: 9765255
SEQUENCE DESCRIPTION: SEQ ID NO: 1475
US-10-641-643-1475
                                                                                                              Query Match 96.6%;
Best Local Similarity 99.8%;
Matches 1321; Conservative
TOPOLOGY: linear IMMEDIATE SOURCE:
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                                   ATTTTGGGGCATTTTTCAGCTTTTTACTTTTGTGAAGGTTTTTTAAACTTGACATCAGAGA
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Susan G. Stuart
Susan G. Stuart
Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: «Unknown»
FILING DATE: «Unknown»
APPLICATION NUMBER: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
RESTERENCE/DOCKET NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 37,071
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-641-643-1475, Sequence 1475, Application US/10641643; Publication No. US20040077003A1; GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1818 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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STATE: CALIFORNIA
COUNTRY: USA
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161 GCGTGGTGCATCAAGTAGAAGGATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC 220  [1] [	TGGCAACTACCCCTTTGACTTCGGGGGCTTCTGGTGGTGGGGGGGCC 5 TCAGCAACTACCCCTTTGACTTCCAGGTGCCAGGGTTCTTTACTGGCCAAGAGGGCC 4 TCAGCAACTACCCCTTTGACTTCCAGGTGCCAGGATCATTACTGGCCAAGAGGAAGGTG 4 TCAGCAACTACCCCTTTTGACTTCCAGGGTGCCAGGATCATTACTGGCGAAGAGGTG 5 CCTATGGCTGGATTACTATCAACTACTGCTGGGGGAAATTCAGTCAG	2 7 9 7	641 CTCTGCAATTTCGCCTCTATGGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGCT 700	761 AAATTCTCAGGGACCCATGCTTTCATCCTGGATATAAGAAGGTAGTAGAAGTGACC 820 [	1014 TCCAGGGTATTGGAAACTATCAAAAGCATCCTGGAGCTCTTCAACCCA 1073 941 GTTACTGCCCTTACTCCCAGGGGCTCTCAAAGGGATTTTCTTGCCACCACTCCAGGGGG 1000	1061   AAGTCTCTCAGGAAAAGTGACTGAGATGATGAAAAGTTCTGTGCTCAGCCTTGGGAGG
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Db   1074 GTTACTGCCCTTACTCCCAGTGTGCCTTCAATGGGATTTTCTTGCCACCACCACCCAGGGGG 1133	Qy         1181 GTACCTACATTCTCCCTCCTTCTGCAAGGCTATCATTTCACAGCTGATTCCTGGAGC 1240           Db         1314 GTACCTACATTCTCTCCCTCCTTCTGCAAGGCTATCATTCACAGCTGATTCCTGGGAGC 1373           Qy         1241 ACATCCATTCATTGGCAAGATCCAGGGCAGCCGGCTGGACTTTGGGCTACATGC 1300           Db         1374 ACATCCATTTCATTGGCAAGATCCAGGGCAGCCGGCTGGACTTTGGGCTACATGC 1300           Db         1374 ACATCCATTTCATTGGCAAGATCCAGGCCACGCCGGCTGGACTTTGGGCTACATGC 1433           Qy         1301 TGAACCTGAACATGATCCCAGGCTACCATTGTCCACTTCCA 1360	Db 1434 TGAACCTGACCTGATCCCAGCTGACCATTGTCCACCACCTCTCCCACTCCA 1493  Qy 1361 CCTA 1364  Db 1494 CCTA 1497  RESULT 7	934-998-290 ence 290, Application US/10934998 ication No. US20050153917A1 tation No. US20050153917A1 LICANT: AL-MAHMOOD, SALMAN LICANT: AL-MAHMOOD, SALMAN LICANT: COLIN, SYLVIE LICANT: SCHNEIDER, CHRISTOPHE LECANTION: GREEN ANVOLVED IN REGILATING ANGIOGENESIS, PHAR	TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF FILE REFERENCE: BMA-04-1206 CURRENT APPLICATION NUMBER: 2014-09-03 PRIOR PAPLICATION NUMBER: PCT/FR03/00695 PRIOR APPLICATION NUMBER: PCT/FR03/00695 PRIOR FILING DATE: 2003-03-04 PRIOR FILING DATE: 2003-03-04 PRIOR FILING DATE: 2002-03-04 PRIOR FILING DATE: 2002-03-04 PRIOR FILING DATE: 2002-03-04 PRIOR FILING DATE: 2002-03-04	NUMBER OF SEQ ID NOS: 301  SOFTWARE: Patentin version 3.2  SOFTWARE: Patentin version 3.2  LEIGHTH: 1818  TYPE: DNA ORGANIZM: Homo sapiens PATABASE ACCESSION NUMBER: Genbank/S73813	Overy Match  Query Match  Best Local Similarity 99.8%; Pred. No. 0;  Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  QY 41 GTTCAACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATGCGGTGGATGCGG 100  Db 174 GGTTGACCCAGAACAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGCTGGATGCGG 233  QY 101 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAG 160  Db 234 GTTCTTCTCACACAAGTTTATACATCTATAAAGTGGCCAGCAGAAAAGGAGAATGACACAG 293

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US-10-240-965-242
Sequence 242, Application US/10240965
; Publication No. US20030165924A1
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APPLICANT: AL-MAHMOOD, SALMAN
APPLICANT: AL-MAHMOOD, SALMAN
APPLICANT: COLIN, SYLVIE
APPLICANT: CCHIN, SYLVIE
APPLICANT: CCHIN, SYLVIE
APPLICANT: CCHIN, SYLVIE
APPLICANT: CHINSIDER, CHINSIONED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL
TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF
FILE REFERENCE: BMA-04-1206
CURRENT PILING DATE: 2004-09-03
PRIOR PELICATION NUMBER: PCT/FR03/00695
PRIOR FILING DATE: 2003-04
PRIOR FILING DATE: 2002-03-04
PRIOR PELICATION NUMBER: FR02/02717
PRIOR PILING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PatentIn version 3.2
SEQ ID NOS: 301
SOFTWARE: PATENTING OF SEQ ID NOS: 301
SOFTWARE: PATENTING OF SEQ ID NOS: 301
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llarity 99.8%; Pred. No. 0;
Conservative 0; Mismatches
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DATABASE ACCESSION NUMBERS: GENBANK/AJ133133
DATABASE ENTRY DATE: 2000-01-19
RELEVANT RESIDUES: (1)..(2081)
                                                                                                                                                              Sequence 46, Application US/10934998; Publication No. US20050153917A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: GS-N45
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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Matches 1321; Conserv
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US-10-934-998-46
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Sequence 147, Application US/10934998

Sequence 147, Application No. US2005015391741

GENERAL INFORMATION:
SALMAN
APPLICANT: AL-MARMOD, SALMAN
APPLICANT: COLIN, SYLVIE
ITILE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL
ITILE OF INVENTION: PREPRATIONS CONTAINING SAME AND APPLICATIONS THEREOF
FILE REFERENCE: BMA-04-1206
CURRENT APPLICATION NUMBER: US/10/934,998
CURRENT FILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: PCT/FR03/00695
PRIOR PLING DATE: 2003-03-04
PRIOR PLING DATE: 2002-03-04
PRIOR FILING DATE: 2002-04-11
PRIOR FILING DATE: 2002-04-11
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   APPLICANT: SHICHMAN, DOV.

APPLICANT: SCHOCYI, Roland
APPLICANT: SCHOCYI, Roland
APPLICANT: SELLHAMN, Richard M.

APPLICANT: SELLHAMN, Richard M.

APPLICANT: SELLHAMS, Jeffrey J.

APPLICANT: PORTER, Gorden J.

APPLICANT: MIKITA, Thomas

APPLICANT: MIKITA, Thomas

APPLICANT: MIKITA, Thomas

TILLE REFERENCE: PA-0025 PCT
CURRENT PLILON WINBER: US/10/240,965

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: 60/195,106

PRIOR FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 276

SEQ ID NO 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4411;
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                                                                                                                                                                                                                                                                                                                       TYPE: DNA
OKGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030165924A1 347965.2
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96.6%; Score 1319.2;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1321; Conservative 0; Mismatches
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GENOMICS, INC
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CCATION: 3369

OTHER INFORMATION: a, t, C,

US-10-240-965-242
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LENGTH: 4411
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Matches 642
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Publication No. US20050153917A1
GENERAL INFORMATION:
APPLICANT: AL-MAHMOOD, SALMAN
APPLICANT: COLIN, SYLVIE
APPLICANT: SCHNEIDER, CHRISTOPHE
TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF
TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF
CURRENT APPLICATION NUMBER: US/10/934,998
CURRENT APPLICATION NUMBER: US/10/934,998
CURRENT APPLICATION NUMBER: PCT/PRO3/00695
PRIOR PILING DATE: 2003-03-04
PRIOR FILING DATE: 2003-03-04
PRIOR APPLICATION NUMBER: FR02/02717
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                                                                                                               Score 640.2; DB 22
Pred. No. 4.3e-193;
0; Mismatches 3;
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NUMBER OF SEQ ID NOS: 301
SOFTWARE: Patentin version 3.2
SEQ ID NO 147
LENGTH: 704
                                                                                                            Query Match
Best Local Similarity 99.5'
Matches 642; Conservative
                                                       TYPE: DNA
ORGANISM: Homo sapiens
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US-10-934-998-193/c
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Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICATT Hyseq, Inc.
TITLE OF INVENTION: PROM VARIOUS cDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT PAPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                             Score 640.2; DB 22
Pred. No. 1.6e-192;
                                                                                                                                                                                                                                                                                       0; Mismatches
PRIOR FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: FR02/04546
PRIOR FILING DATE: 2002-04-11
NUMBER: OF SEQ ID NOS: 301
SOFTWARE: Patentin version 3.2
SEQ ID NO 193
LENGTH: 6164
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al Similarity 99.5%;
642; Conservative (
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US-09-918-995-24656
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; ORGANISM: HOMO
US-10-934-998-193
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| Publication No. US20030157486A1
| GENERAL INFORMATION:
| APPLICANT: Graff. Jonathon M.
| APPLICANT: Mucheer, Matthew
| TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES
| FILE REFERENCE: A34943 0904955.0243
| CURRENT APPLICATION NUMBER: US/10/002,631C
| CURRENT FILING DATE: 2001-10-31
| PRIOR PILING DATE: 2001-06-21
| NUMBER OF SEQ ID NOS: 324
| SOFTWARE: FastSEQ for Windows Version 4.0
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: LOCATION: (656)...(698)

: CTHER INFORMATION: n = A, C,

US-10-002-631C-275
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Best Local Similarity 80.2
Matches 394; Conservative
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US-10-002-631C-275/c
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LENGTH: 703
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                                                                                                                                                                            Length 475;
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; Sequence 23052, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
    APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: NOVEL NUCLEIC CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT PLING DATE: 1999-01-20
; PRIOR PILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FEGLSEQ for Windows Version 3.0
; SEQ ID NO 23052
LENGTH: 484
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Pred. No. 6.3e-121;
0; Mismatches 15;
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 24656
LENGTH: 475
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LOCATION: (1)...(484)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 96.6%;
Matches 423; Conservative
                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-24656
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ORGANISM: Homo sapiens
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US-09-918-995-23052
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                             CCAGCCCTTTGACTTTTAGGGGTGCTCAAATCATTTCTGGGCAAGAAGAAGAGGGGTATATGG
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Job time : 993.919 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KATZ, RUTH
APPLICANT: XATZ, RUTH
APPLICANT: JIANG, FENG
TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS
FILE REFERENCE: UTSC.658US
CURRENT APPLICATION NUMBER: US/09/923,304
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
LENGTH: 2797
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54.3%; Pred. No. 3.7e-81;
ive 0; Mismatches 575; Indels
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Matches 707; Conservative
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ORGANISM: Homo sapiens
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; LOCATION: (83)..(1672)
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AF005940 Bos tauru
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AX828501 Sequence
AX82851 Sequence
AX828547 Xenopus 1
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C12N15/09,A61K38/00,A61P9/00,C07K14/705,C12N1/15,C12N1/19, PC
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BD228700.1 GI:33038470

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PI CHARLES R MALISTERMENT
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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TITLE
JOURNAL
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                           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum DB seq length: 200000000
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GCATTTTCAGCTTTTTACTTTGTGATGAGCTTTTTAAACTTGACATCAGAGAAAGTCTCT 1140
                                                                                    ATTCTCTCCCTCCTTCTGCAAGGCTATCATTTCACAGCTGATTCCTGGGAGCACATCCAT 1320
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by JP 2002527096-A/13
pp 27-AUG-2002
pp 13-OCT-1999 JP 2000577185
pr 16-OCT-1999 US 60/104585,06-NOV-1998 US 60/107466 PR
pr 13-AUG-1999 US 60/149010
pr 13-AUG-1999 US 60/149010
pr CHARLES R MALISZEWSKI, RICHARD B GAYLE III, VIRGINIA L PRICE,
STEVEN D GIMPEL
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                                                                                                                                                ATTCTCTCCTCCTTCTGCAAGGCTATCATTCACAGCTGATTCCTGGGAGCACATCCAT
                                            1 ATGCCCCTGTGGATCGACAGGATGCAACTCCTGTCTTGCATTGCACTAAGTCTTGCACTT
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I laistewski, C.R., Iii, R.B.G., Price, V.L. and Gimpe, S
Inhibitors of platelet activation and recruitment
I Patent: JP 2002527096-A 13 27-AUG-2002;
IMMUNEX CORP
OS Artificial Sequence
PN JP 2002527096-A/13
PD 27-AUG-2002
PF 13-OCT-1999 JP 2000577185
PR 13-OCT-1999 US 60/104585,06-NOV-1998 US 60
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97.4%; Score 1400; DB 6;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1437; Conservative 0; Mismatches 0;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_rref="taxon:32630"
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PC C12P2'
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                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo. (Dases 1 to 1599)
Maliszewski, C.R., Iii, R.B.G., Price, V.L. and Gimpe, S.D. Inhibitores of platelet activation and recruitment
Patent: JP 2002527096-A 1 27-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                 ON THOSE SECTION (ALCONOMINATE)

PN JP 2002527096-A/1

PD 27-AUG-2002

PP 13-OCT-1999 JP 2000577185

PR 16-OCT-1999 US 60/104585,06-NOV-1998 US 60/107466 PR

13-AUG-1999 US 60/149010

PI CHARLES R MALISZEWSKI, RICHARD B GAYLE III, VIRGINIA L PRICE,
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Inhibitors of platelet activation and recruitment FH
Location/Qualifiers
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Inhibitors of platelet activation and recruitment.
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99.8%; Pred. No. 0;
:ive 0; Mismatches
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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JP 2002527096-A/1.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 99.8
Matches 1321; Conservative
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Kaczmarek, E., Koziak, K., Sevigny, J., Siegel, J.B., Anrather, J., Beaudoin, A.R., Bach, F.H. and Robson, S.C.

Biret Submission

Submitted (30-JAN-1997) Medicine, Harvard University, 99 Brookline Avenue, BIDMC, RN, Boston, MA 02215, USA

Location/Qualifiers

1. 1704

//organism=Homo sapiens"

//db_xrefe="mxNA"

//db_xrefe="taxon:9606"
                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 1704)

Kaczmarek, E., Koziak, K., Sevigny, J., Siegel, J.B., Anrather, J., Beaudoin, A.R., Bach, F.H. and Robson, S.C.
Identification and characterization of CD39/vascular ATP
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Robson,S.C., Kaczmarek,E., Siegel,J.B., Candinas,D., Koziak,K., Millan,M., Hancock,W.W. and Bach,F.H.
Loss of ATP diphosphohydrolase activity with endothelial cell
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91.8%;
Best Local Similarity 99.8%;
Matches 1321; Conservative 0 257 293 요 ò

linear

PRI 18-FEB-1997

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RESULT 5 HSU87967 LOCUS DEFINITION ACCESSION

1704 bp mRNA linea Human ATP diphosphohydrolase mRNA, complete cds. U87967

143 145 6 53 TION ION N N DS	SOURCE Unknown.  ORGANISM Unknown.  DOLJABSHÍTÍGG.  REFERENCE 1 (bases 1 to 1818)  AUTHORS Beaudoin, A.R. and Sevigny, J.  TILLE Mammalian ATP-diphosphohydrolases and process of purification  TILLE Patent: US 6287837-A 2 11-SEP-2001;  FEATURES Location/Qualifiers  SOURCE /organism="unknown"  /mol_type="unassigned DNA"	91.8%;   Score 1319.2;   DB 6;   Length 1818;	Db 234 GTTCTTCTCACACAAGTTTATACTTCTATAGTGGCCAGCAGAAAAAGGAGAAAAAAGGAGAAAAAGGAGAAAAAGGAGA	353 TTCCAAGGTCCCAGCACAAGAACACCCGTTTACCTGGGAGCCACGCCAGGCATGCGGT  414 TTCCAAGGTCCCAGCACACAGAAGACACCCGTTTACCTGGGAGCCACGCCAGGCATGCGGT  415 TGCTCAGGATGGAAAGTCAAGAGATTGGCAGACCTTCTGGATGTGGTGGTGGAGGCAGGC	Db   534   TCAGCAACTACCCCTITICACTACCAGGGGGGCAACTACTGGCCAAGAGGGGGCAAGAGGGGGCAAGAGGGGGCAAGAGGGGGCAAGAGGGGGCAAGAGGGGGCAAGAGGGGGCAAGAGGGGGG
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Matches   131;   Conservative   0;   Wismatches   3;   Indels   0;   Gaps   0;   Gaps   13   3   3   3   3   3   3   3   3	833 AAATTCTCAGGACCCATGCTTTCATCTGGATATAGAAGTAGTGAACTAGTGCC 894 AAATTCTCAGGACCCATGCTTTCATCCTGGATATAAGAAGGTAGTGAACTGACCC 895 TTTACAAGACCCCTGCACCAAGAGATTTGAGATGACTCTTCCATTCCAGCAGTTTGAAA 9 897 TTTACAAGACCCCTGCACCAAGAGATTTGAGATGACTCTTCCATTCCAGCAGTTTGAAA 1 958 TTTACAAGACCCCCTGCACCAAGAGATTTGAGATGACTCTTCCATTCCAGCAGTTTGAAA 1 959 TCCAGGGTATTGGAACTATCAACAATGCCATCCAAGAGCTCTTCCACCCA 1 1014 TCCAGGGTATTGGAACTATCAACAATGCCATCCAAGAGCTCTTCAACACCA 1 1015 GTTACTGCCCTTACTCCCAGTGTGCCTTCAATGGGATTTTCTTGCCACCCCCTCCAGGGGG 1 1017 GTTACTGCCCTTACTCCCAGTGTGCCTTCAATGGGATTTTCTTGCCACCCCCCCC
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            534 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGAGGTG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Genes involved in regulating angiogenesis, pharmaceutical
preparations containing same and applications thereof
Patent: WO 0374073-A 290 12-SEP-2003;
Gene Signal (FR)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 290 from Patent WO03074073.
AX828644
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99.8%; Pred. No. 0;
tive 0; Mismatches
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/product="1"ymphoid cell activation antigen"
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TLGYMLNLTNMIPABQPLSTPLSHSTYVFLMVLFSLVLFTVAIIGLLIFHKPSYFWKD
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CD39=lymphoid cell activation antigen (human, B lymhpoblastoid cell
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Maliazewski,C.R., Dalespesse,G.J., Schoenborn,M.A., Armitage,R.J.,

Panslow,W.C., Nakajima,T., Baker,E., Sutherland,G.R.,

Poindexter,K., Birks,C. et,al.

Poindexter,K., Birks,C. atial.

Structural characterization antigen. Molecular cloning and structural characterization

J. Immunol. 153 (8), 3574-3583 (1994)
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entry (NCBI gibbsq 156681) from the original journal article.
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/note="lymphoid cell activation antigen, CD39"
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Homo sapiens mRNA for ecto-ATP diphosphohydrolase, isolate C1800.
AJ133133
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The cDNA cloning of human placental ecto-ATP diphosphohydrolases I and II
PEBS Lett. 453 (3), 335-340 (1999)
99332082
971 ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAGGACATTCAGGTTGCAAGTAATG 1030
                           AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTGGGAGG 1192
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ecto-ATPDase I; ecto-ATPDase I; PleA 1 gene.
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Homo sapiens
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Submitted (23-FEB-1999) Matsumoto M., Department of Blood
Transfusion Medicine, Nara Medical University, Kashihara,
Nara,634-8522, JAPAN
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Matsumoto, M.
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                                                                                                         Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                             Al-Mahmood,S., Colin,S. and Schneider,C.
Genes involved in regulating angiogenesis, pharmaceutical
preparations containing same and applications thereof
Patent: WO 0307403-A 46 12-SRP-2003;
Gene Signal (FR)
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                  DNA
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99.8%; Pred. No. 0;
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          2081 bp
Sequence 46 from Patent WO03074073.
AX828400
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/db_xref="taxon:9606"
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                                                             AX828400.1 GI:39838400
                                                                                        Homo sapiens (human)
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Matches 1321; Conservative
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                       AAATTCTCAGGGACCCATGCTTCATCCTGGATATAAGAAGGTAGTGAACGTAAGTGACC
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                                                                ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAGGACATTCAGGTTGCAAGTAATG
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    CTCTGCAATTTCGCCTCTATGGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGCT
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Novel therapeutic targets in cancer
Patent: WO 20040/73120-A 693 02-SEP-2004;
Sagres Discovery, Inc. (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
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                                                                                                                                                 / Function="apyrass=""
// function="apyrass=""
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// codon_geart=1
// produc_t="ecto-ATP diphosphohydrolase I"
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// QSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFLMVLFSLVLFTVAIIGLLIPHK
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Pred. No. 0;
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/db_xref="taxon:9606"
/tissue_type="placenta"
                 sapiens"
                                                                                                       184. .1737
/gene="PleA 1"
/EC_number="3.6.1.5"
                                                                                          /gene="PleA 1"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Morris,D.W., Morris,D.W. and Malandro,M.S.
Novel therapeutic targets in cancer
Patent: WO 2004074320-A 697 02-SEP-2004;
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Sequence 697 from Patent WO2004074320.
CQ870276
CQ870276.1 GI:519998R0
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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Best Local Similarity 99.8%;
Matches 1321; Conservative 0
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Homo sapiens (human)
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Pred. No. 0;
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Score 1319.2;
Pred. No. 0;
0; Mismatches
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99.8%;
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Best Local Similarity 99.8
Matches 1321; Conservative
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AAD00207 standard; DNA; 1437 BP.

RESULT 1 AAD00207

Soluble CD39; solCD39; human; apyrase activity; platelet activation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; bVT; pulmonary embolism; PE; thrombos formation; occlusion; restenosis; angiogenesis; antianginal; cerebroprotective; antitorablan; cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; ds. /\*tag= d /note= "Linker sequence" 118. .1434 /\*tag= e /note= "Coding region of human soluble CD39 (solCD39)" "Mature human interleukin 2 N-terminal end" l. .72 /\*tag= b /note= "Human interleukin 2 (hIL2) leader sequence" "Fusion protein of pIL2LsolCD39" Human soluble CD39 fusion DNA construct, pIL2LsolCD39. Location/Qualifiers 1. .1437 /\*tag= a /product= " (first entry) /product= 109. .117 \*tag= c .108 Homo sapiens. Synthetic. misc\_feature misc\_feature misc\_feature 17-AUG-2000 sig\_peptide AAD00207; Key  N

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99US-0149010P.
99WO-US022955
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13-OCT-1999;
                                        16-OCT-1998;
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13-AUG-1999;
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The present sequence is coding region of pIL2SolCD39, a fusion construct encoding acl (soluble)(CD39 having apyrase activity. Fusion of 12 amino acids from the N-terminus of mature human IL2 to the solCD39 coding region results in high levels of both expression and activity in the supernatants of transfected cells. This is used in the treatment of unstable angina, myocardial infartion, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, platelet-associated ischaemia ciscoder including lung ischaemia, coronary ischaemia and cerebral ischaemia, thrombosis, disorder including coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis,
                                                                                                            unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated isohaemic disorder; lung ischaemia; thrombolytic; cerebral ischaemia; thrombolic disorder; coronary artery thrombosis; cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis; peripheral artery thrombosis; coagulopathy; deep venous thrombosis; psripheral artery thrombosis; coagulopathy; deep venous thrombosis; psripheral artery thrombosis; ransient ischaemic attack; thrombus formation; occlusion; stenosis; restenosis; antianginal; cardiant; cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant; coronary ischaemia; vascular occlusion; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibiting platelet activation and recruitment, useful for treating a mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD39 polypeptides.
                                                                                              Soluble CD39; ADP-induced platelet activation; platelet aggregation;
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*tag= a
product= "Fusion construct of pIL2Lsol
1. .72
*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mature human IL2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                    "human IL2 leader sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    three amino acid linker'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "Soluble CD39 protein"
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                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                 Coding region of pIL2Lsol CD39.
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The present DNA sequence is a fusion construct pIL2IrFlagSolCD39, comprising the leader peptide of human interleukin 2 (hIL2), 12 amino acids from the mature N-terminus of hIL2, a linker, FLAG tag sequence and soluble CD39 (solCD39) coding region, that has apyrase activity. This produces high levels of solCD39 sepression and activity in the cranisacted calls. Soluble CD39 is constructed by removing the N- and C-terminal transmembrane domains. It retains the capacity to metabolise ATP and ADP at relevant concentrations and the ability to block and reverse ADP-induced platelet activation and recruitment, including platelet aggregation. Soluble CD39 polypeptides are useful for inhibiting angiogenesis. It is useful for the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, capacites, peripheral vascular occlusion, precelampsia, embolism, clastelet-associated ischaemic disorders including coronary and cerebral artery thrombosis, intracactiac and venous thrombosis, coagulopathy, deep venous thrombosis, intracactiac and venous thrombosis. Coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and thrombosis or transient ischaemic attack. Soluble CD39 is also useful for preventing chrombosis or thrombosis 
145. .1461
/*tag= e
/note= "Coding region of human soluble CD39 (solCD39)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 GAAAAGGAGAATGACACAGGGGTGGTGCATCAAGTAGAAGAATGCAGGGTTAAAGGTCCT
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Pred. No. 0;
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Best Local Similarity 98.2%; Pred. No. 0;
Matches 1437; Conservative 0; Mismatches
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P-PSDB; AAY70921.
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  901 ACCCCCTGCACCAAGAGATTTGAGATGACTCTTCCATTCCAGCAGTTTGAAATCCAGGGT 960
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product= "Fusion protein of pIL2LFlagSolCD39"
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              1381 TGGACTTTGGGCTACATGCTGACCTGACCAACATGATCCCAGCTGAGCAACCATTGTCC
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product= "SolCD39 expression plasmid protein"
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                                                                                                                                                                                                                                          region of soluble CD39 expression plasmid.
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*tag= a
note= "huIL2 leader sequence"
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/note= "Flag tag"
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mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD39 polypeptides.
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Example 9; Page 107-109; 118pp; English.

The present sequence is the coding region of soluble CD39(solCD39) expression plasmid. This was used for the transient expression of solCD39 protein in mammalian expression systems. SolCD39 is used in the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, platelet-associated ischaemic disorder including lung ischaemia, coronary ischaemia and cerebral ischaemia, a thrombotic disorder including coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis (DVT), thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, recoclusion, stenosis or restenosis of blood vessels or stroke 

Seguence 1464 BP; 424 A; 340 C; 342 G; 358 T; 0 U; 0 Other;

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213 240 300 360 GCCACGCCAGGCATGCGGTTGCTCAGGATGGAAAGTTGAAAGATTGGCAGACAGGGGTTCTCTG 480 540 573 900 9 693 GTCACAAACAGTGCACCTACTTCAAGTTCTACAAAGAAAACACAGCTAACTAGTTC---- 116 GTCACAAACAGTGCACCTACTTCAAGTTCTACAAAGAAAACACAGGTAACTAGTTCAGGA 120 180 273 333 393 GCCACGGCAGGCATGCGGTTGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTG 453 513 633 9 9 -------AACCCAGAACAAAGCATTGCCAGAAAAGTAT GACTACAAAGATGACGATGACAAAACCCAGAACAAAGCATTGCCAGAAAAGTTAAGTAT GAAAAGGAGAATGACACAGGCGTGGTGCATCAAGTAGAAGAATGCAGGGTTAAAGGTCCT GAAAGAGCTAGGGAAGTGATTCCAAGGTCCCAGCACCAAGAGACACCCGTTTACCTGGGA ACTGGCCAAGAGGAAGGTGCCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAATTC GGGATTGTGCTGGATGCGGGTTCTTCTCACAGTTTATACATCTATAAGTGGCCAGCA GGGATTGTGCTGGATGCGGGTTCTTCTCACACAGTTTATACATCTATAAGTGGCCAGCA GATGTGGTGGAGAGGCCTCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATT AGTCAGAAAACAAGGTGGTTCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTT 1 ATGGCCCTGTGGATCGACAGGATGCAACTCCTGTCTTGCATTGCACTAAGTCTTGCACTT ATGCCCCTGTGGATCGACAGGATGCAACTCCTGTCTTGCATTGCACTAAGTCTTGCACTT GAAAAGGAGAATGACACAGGCGTGGTGCATCAAGTAGAAGAATGCAGGGTTAAAGGTCCT GATGTGGTGGAGAGAGCCTCAGCAACTACCCCTTTTGACTTCCAGGGTGCCAGGATCATT GGAGCTTTGGACCTTGGGGGAGCCTCTACACAAGTCACTTTTGTACCCCCAAAACCAGACT Gaps 27; 97.4%; Score 1400; DB 3; Length 1464; 98.2%; Pred. No. 0; 0; Indels 0; Mismatches 98.2%; Best Local Similarity 98.2 Matches 1437; Conservative 61 61 117 121 154 181 241 301 361 454 514 634 Query Match 214 274 334 394 421 481 541 574 601

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present DNA sequence is a fusion construct, comprising the N-terminal region of mature human interleukin2 (IL2) and soluble CD39 (solCD39) coding region, having apyrase activity. This results in high levels of solCD39 expression and activity in the transfected cells. Soluble CD39 is constructed by removing the N- and C-terminal transmembrane domains. It retains the capacity to metabolise ATP and ADP at relevant concentrations and the ability to block and reverse ADP-induced platelet activation and recruitment, including platelet aggregation. Soluble CD39 polypeptides recruitment, including platelet aggregation. Soluble CD39 polypeptides or injury, atherosclerosis, peripheral vascular occlusion, precelampsia, cunstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, precelampsia, coronary and cerebral ischaemia, thrombosis intracardiac and venous peripheral and crebral artery thrombosis intracardiac and venous thrombosis, companism (PE) and transient ischaemic attack. Soluble CD39 is also useful CD2 preventing thrombosis formation, occlusion, reocclusion,
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                                                                                                                                                                           /notes "N-terminus of mature human interleukin 2 (IL2)" 46.\ .1362 /*tag= c
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                                          The present cDNA sequence is a fusion construct encoding sol(soluble)CD39 having apyrase activity. Fusion of 12 amino acids from the N-terminus of mature human IL2 to the solCD39 coding region results in high levels of both expression and activity in the supernatants of transfected cells. This is used in the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, precelampsia, embolism, platelet-associated ischaemic disorder including lung ischaemia, coronary ischaemia and cerebral ischaemia, a thrombotic disorder including coronary artery thrombosis,
                                                                                                                                                                                                                                                                                                                                                                                                                       Soluble CD39; ADP-induced platelet activation; platelet aggregation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; lung ischaemia; thrombolytic; cerebral ischaemia; thrombosis; cerebral artery thrombosis; intracardiac thrombosis; nerons thrombosis; peripheral artery thrombosis; cogquiopathy; deep venous thrombosis; peripheral artery thrombosis; restenness thrombosis; DVF; PB; pulmonary embolism; transient ischaemic attack; thrombus formation; cecclusion; secoclusion; secoclusion; secoclusion; secoclusion; cecclusion; secoclusion;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibiting platelet activation and recruitment, useful for treating a mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD39
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                                                                                                                                                         DB 3; Length 1365;
                                                                                                                 Sequence 1365 BP; 394 A; 317 C; 319 G; 335 T; 0 U; 0 Other;
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                                                                                                                                                       95.0%; Score 1365; Dilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
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Matches 1365, Conserv
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The present sequence is the cDNA encoding the human soluble CD39 protein, a cell surface molecule, having apyrase activity. It is derived from a human B cell line cDNA library, referred to as MP-1. Soluble CD39 is constructed by removing the N- and C-terminal transmembrane domains. It retains the capacity to metabolise ATP and ADP at relevant concentrations and the ability to block and reverse ADP-induced platelet activation and recuritment, including platelet aggregation. Soluble CD39 polypeptides are useful for inhibiting angiogenesis. It is useful for the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, precolampsis, embolism, platelet-associated ischemic disorders including lung, coronary and cerebral ischaemia, thrombotic disorders including coronary, coronary and cerebral artery thrombotic disorders including coronary, thrombosis, intracardiac and venous thrombosis, coagulopathy, deep venous thrombosis (UVI), pulmonary embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion,
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Pred. No. 0;
0; Mismatches
                                                                                                                                                   Example 9; Page 85-87; 122pp; English
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99.8%; Pred
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Matches 1321; Conservative
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                   WPI; 2000-339644/29.
P-PSDB; AAY70910.
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                                                                                                                                                                        1021 TITIACTITIGIAGAAGTITITAAACTIGACATCAGAGAAAGGTGT
                     CAACAATGCCATCAAAGCATCCTGGAGCTCTTCAACACCCGGTTACTGCCCTTACTCCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "Human soluble CD39
/note= "Cell surface molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human soluble CD39 protein encoding cDNA
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The present cDNA sequence encodes soluble CD39 having apyrase activity.

This was derived from a cDNA library prepared from a human B cell line

creferred to as MP-1. Soluble CD39 retains the capacity of wildtype CD39

to metabolise ATP and ADP at physiologically relevant concentrations as

creding as the ability to block and reverse ADP-induced platelet activation

and recruitment including platelet aggregation. This is used in the

creatment of unstable angina, myocardial infarction, stroke, coronary

cartery disease or injury, atherosclerosis, peripheral vascular occlusion,

creatment, coronary ischaemia and carebral ischaemia, a thrombotic

clingischaemia, coronary artery thrombosis, cerebral ischaemia, a thrombotic

clisorder including coronary artery thrombosis, cerebral artery

thrombosis, intracardiac thrombosis, peripheral artery thrombosis, thrombosis, coagulopathy, deep venous thrombosis, venous

thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT),

culmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also

cuseful for preventing thrombus formation or reformation, occlusion,

crecclusion, stenosis or restenosis of blood vessels or stroke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 GITCAACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGCGG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibiting platelet activation and recruitment, useful for treating a mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD39 polypeptides.
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cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant; coronary ischaemia; vascular occlusion; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.8%; Score 1319.2; DB 3; Length 1599; 99.8%; Pred. No. 0; 1.00 0; Mismatches 3; Indels 0;
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                                                                                                                                                     protein"
                                                                                                                                                     "Soluble CD39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 10; Page 85-87; 118pp; English.
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                                                                                              Location/Qualifiers
67. .1599
                                                                                                                                                                                                                                                                                                                                                                            (IMMV ) IMMUNEX CORP.
(CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                      98US-0104585P.
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99US-0149010P.
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P-PSDB; AAY70887.
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                                                          Homo sapiens
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                                                                                                                                                                        AAATTCTCAGGGACCCATGCTTTCATCCTGGATATAAGAAGGTAGTGAACGTAAGTGACC 892
                                                                                                                                                                                                TTTACAAGACCCCCTGCACCAAGAGATTTGAGATGACTCTTCCATTCCAGCAGTTTGAAA 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soluble CD39; ADP-induced platelet activation; platelet aggregation; unstable angina; myocardial infarction; stroke; coronary artery disease; atheroselerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; lung ischaemia; thrombotic; cerebral ischaemia; thrombotic disorder; coronary artery thrombosis; cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis; peripheral artery thrombosis; ocaqulopathy; deep venous thrombosis; DVT; PE; pullmonary embolism; transient ischaemic attack; thrombos formation; occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant;
                                                                                                                     ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAGGACATTCAGGTTGCAAGTAATG
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                                           AAGTCTCTCAGGAAAAGGTGACTGAGATGAAAAAATTCTGTGCTCAGCCTTGGGAGG
                                                                                                  ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAGGACATTCAGGTTGCAAGTAATG
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4-1BB; CD30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a method of treating cardiovascular disease in a subject, comprising administering an IL-17, IL-18, 4-1BB, CD30 or OX40 antagonist. The IL-17, IL-18, 4-1BB, CD30 or OX40 antagonists are useful for treating cardiovascular disorders, e.g. chronic immune) myocarditis, congestive heart failure, aneurysms, angina, embolism, restenosis, ischaemia or thrombocytopenic purpura. T present sequence is a coding sequence used in the exemplification of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTCTTCTCACACATTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAG
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                                                                                                                                                                                                                  ene; cardiovascular disease; IL-17; interleukin; IL-18;
antagonist.
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Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                                                                                                                     Location/Qualifiers
67. .1599
/*tag= a
/product= "CD39"
                                                                                                      BP.
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                                                                                                      ADL24294 standard; DNA; 1599
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12-AUG-2003; 2003US-0494457P.
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99.8%;
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                                                                                                                                                                                              Human CD39 coding sequence
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CCTA 1436
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                        CCTA
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OX40; anta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method for increasing or decreasing drug resistance in target bacteria, yeast, plant or mammalian cells by altering the ATP gradient across the biological membrane of the target cell. The method is useful for modulating drug resistance of cells. It iuseful for increasing the sensitivity of cells to chemotheraputic and antibiotic agents and increasing resistance to herbicides. The present sequence is human ATP diphosphohydrolase coding sequence. This sequence encodes was used in the present invention to modulate drug resistance. Note: The present sequence is not shown in the specification, but is referred to via its GenBank accession number
                             1433 TGAACCTGACCAACATGATCCCAGCTGAGCAACCATTGTCCACACCTCTCTCCCACACCTCT
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1321; Conservative 0; Mismatches
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The invention relates to a conjugate (1) comprising an enzyme and a biodegradable polymer, where (i) enzymatic activity of the enzyme is biodegradable polymer, where (i) enzyme in the absence of the biodegradable polymer, or (ii) the half life of the enzyme is longer than that of the colymer, or (ii) the half life of the enzyme is longer than that of the colymer. The enzyme is longer than that of the colymer. The enzyme is a multimeric, soluble and/or extracellular mazyme, colymer. The enzyme especially a soluble form of CD39 and catalyzes hydrolysis of nucleoside diphosphate. The conjugate can be used to treat abnormal aggregation of platelets, particularly cardiovascular disease.

C diseases relating to abnormal levels of extracellular nucleotides or abnormal aggregation of platelets, particularly cardiovascular disease, cancer, sepsis or a disease related to graft transplant. (1) is also used infarction, unstable angina, atherosclerosis, pre-eclampsis, embolism, claretelet associated ischaemic disorders including lung, coronary and cerebral ischaemia, reocclusion following thrombosis, thrombotic cascers, and thrombosis and coagulopathies associated with exposure to a foreign or injured tissue surface, in combination with angioplasty, carctid endarterectomy, anastomosis of vascular grafts and chronic cardiovascular devices. The present sequence represents a DNA encoding a 1456 1397 TGAACCTGACCAACATGATCCCAGCTGAGCAACCATTGTCCACACCTCTCTCCCACTCCA New enzyme polymer conjugate used for treating abnormal levels of extracellular nucleotides or platelet aggregation, graft transplant, cardiovascular disease, cancer and sepsis. CD39; nucleoside diphosphate; thrombolytic; anticoagulant; cardiovascular; cytostatic; antibacterial; immunosuppressive; cardiant; antianginal; antiarteriosclerotic; gynaecological; cerebroprotective; cancer; human; apyrase; gene; ds.

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The bovine aorta (AAW04335 to AAW04338 and AAW04340) and porcine pancreatic (AAW04339) ATPDases have been partially sequenced. The sequences have been found to be highly homologous to a human lymphoid cell activation antigen designated CD39 (Waliszenski et at. (1994). J. Immunol.: 3574-3583). The complete sequences of the ATPDases types I and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated ATP di:phospho:hydrolase enzymes - have anti-haemostatic
activity, useful for reducing platelet aggregation and thrombogenicity
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                                                                                    Gaps
                                                          Length 1704;
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                                Sequence 1704 BP; 468 A; 392 C; 403 G; 441 T; 0 U; 0 Other;
                                                                                    3; Indels
                                                         DB 10;
                                                        Score 1319.2;
Pred. No. 0;
0; Mismatches
                                                      vuery Match
Best Local Similarity 99.8%;
Matches 1321; Conservative
     polypeptide.
     human CD39
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/EC_number= "3.6.1.5"
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                                                                                                                                                                                                                                                                                                                 1194 AAGTCTCTCAGGAAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTGGGAGG
                                                                                                                                                             AGATAAAAACATCTTACGCTGGAGTAAAAGGAGAAGTACCTGAGTGAATACTGCTTTTCTG
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     1074 GTTACTGCCCTTACTCCCAGTGTGCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGG
                                 ATTTTGGGGCATTTTCGCGTTTTTACTTTGTGATGAAGTTTTTAAACTTGACATCAGAGA
                                                  1134 ATTTTGGGGCATTTTCAGCTTTTTACTTTGTGAAGTTTTTAAACTTGACATCAGAGA
                                                                                       AAGTCTCTCAGGAAAAGGTGACTGAGATGAAAAAGTTCTGTGCTCAGCCTTGGGAGG
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II have not been obtained yet. Assuming that the CD39 gene product is an ATDBASE type II, the use of CD39 in the reduction of platelet aggregation and of thrombogenicity may be contemplated, as well as a process of making ATPDASSE using the CD39 sequence (AAT38516)
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                                                                        Sequence 1818 BP; 494 A; 418 C; 433 G; 473 T; 0 U; 0 Other;
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                               954 ITTACAAGACCCCCTGCACCAAGAGATTTGAGATGACTCTTCCATTCCAGCAGTTTGAAA
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                                                                                  Non-human transgenic or somatic recombinant mammals, whose cells contain a heterologous DNA encoding a polypeptide (especially human CD39 protein) having ATP-diphosphohydrolase activity under cellular activating conditions is claimed. In particular the animal is a pig and its cells (or tissues or organs) can be used for transplantation. DNA coding for human CD39 is also useful for genetically modifying a mammalian cell to render it less susceptible to an inflammatory or immunological stimulus and platelet aggregation. The modified cells can be used to prevent or alleviate a thrombotic condition. The present sequence encodes human CD39 protein and was disclosed in J.Immunol. 153 (8) (1994) 3574-3584
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for preventing or alleviating thrombotic condition in
                                                                                                                                                                                                                                                                                      Sequence 1818 BP; 494 A; 418 C; 433 G; 473 T; 0 U; 0 Other;
                                                  Page 38; 65pp; English
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A composition comprising a plurality of cDNAs, useful for detecting altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma or osteoarthritis.

SEQ ID NO 1475; 50pp; English.

The invention relates to a composition comprising a plurality of CDNAs for detecting the altered expression of genes in an immunological response. The invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, comprising obtaining nucleic acids from a sample, contacting the invention of an immunopathological conditions to form one or more hybridisation complexes, detecting the hybridisation complexes and comparing the levels of the detected in complexes with the level of hybridisation complexes with the level of hybridisation complexes with the level of hybridisation complexes or more hybridisation complexes with the level of hybridisation complexes or more hybridisation complexes or more hybridisation complexes with the level of hybridisation complexes or more hybridisation complexes or more hybridisation complexes or more hybridisation complexes or correlates with the presence of the discovers of the discovers and a comparison of proposed are an expression profile comprising a microarray of polynucleotide probes. The General or method for identifying a plurality of polynucleotide probes. The converse or method for identifying a plurality of polynucleotide probes. The converse of the diagnosis of an immunopathology, such as Crohn's disease, asthma, culcerative colitis, hypereosinophila, irritable bowel syndrome, carcinogenic frumesticing architicis or acute monocytic leukaemia, and in identifying agents for the treatment of the diseases. The microarray may also be used in drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. The composition carcinogenic fragments. This sequence represents a human cDNA of the invention. Note: The sequence fate for this patent dor form part of the printing proposition has because the printined appears the presence of the carcinogenic format directly when the presence of the carcinogenic format directly when the presence of the carcinogenic format directly when th from USPTO at segdata.uspto.gov/seguence.html 

Sequence 1818 BP; 494 A; 418 C; 433 G; 473 T; 0 U; 0 Other;

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ö 413 233 232 353 352 412 472 592 GTTCAACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGCGG 172 473 533 593 653 TCAGCAACTACCCCTTTGACTTCCAGGTGCCAGGATCATTACTGGCCAAGAGGAGGTG GTTCTTCTCACACAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAG GTTCTTCTCACACACATTATACATCTATAAGTGGCCAGCAGAAAAAGGAGAATGACACAG GCGTGGTGCATCAAGTAGAAGAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC GCGTGGTGCATCAAGTAGAAGAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGGGAAGTGA AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGGGAAGTGA TGCTCAGGATGGAAAGTGAAGATTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGAGCC TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGGAGGAAGGTG Gaps 91.8%; Score 1319.2; DB 11; Length 1818; 99.8%; Pred. No. 0; 99.8%; ive 0; Mismatches 3; Indels 0; Best Local Similarity 99.8 Matches 1321; Conservative 113 174 173 234 233 294 293 354 414 474 473 534 594 353 533 413

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                     474 TGCTCAGGATGGAAAGTGAAGAGTTTGGAGGTTCTGGATGTGGAGAGGAGGCCC
                                                                                                      TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGAAGGTG
                                                                                                                                                                                                                                                                         TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTGGGG
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TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGAGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel pharmaceutical composition active on angiogenesis comprising an endothelial cell nucleic acid whose expression is induced by an angiogenic factor and inhibited by an angiostatic agent or its complement or fragment, a polypeptide sequence encoded by the nucleic acid or its fragment, a molecule capable of inhibiting expression of the nucleic acid or a malecule which binds to the polypeptide angiogenic. The invention is used to diagnose, prognose or treat an angiogenic disorder in a mammal, particularly a human. The disorder is angiogenic disorder in a mammal, particularly a human. The disorder is confined and the angiogenic disorder in a relational and a nucleic angiogenic disorder in a mammal, particularly a human. The disorder is confined and a second at the second and a relation and a partipleral vacular disease, hypertinaion, vascular inflammation, restenosis due to ancular disease, hypertension, chronic heart disease, ardiac congestion or macular degeneration due to age or osteoporosis. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Compositions for diagnosing, prognosing and treating angiogenic disorders including tumor vascularization and heart disease, comprise nucleic acid or polypeptide differentially expressed in angiogenesis.
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antiinflammatory; cardiant; angiogenesis inhibitor; gene therapy; angiogenesis; endothelial cell; diagnosis; tumor vascularization; retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis.
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.8%;
Matches 1321; Conservative
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AL MAHMOOD S
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Search completed: September 21, 2005, 17:05:32 Job time : 832.224 secs

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Genoscope.

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

18t strand cDNA was primed with a NoLI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTC 21-JUL-2004
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BP434198
AGENCOURT
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BP170602
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AL572575
602926181
BP170295
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Eukaryotani
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 1760)
Li,W.B.; Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
                                                                                                      BP141351
BP157197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels 122; Gaps
                                                            BP464335
BP141657
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BP1511951
BP151197
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BP434894
BP434894
BP434894
BP434894
BP635857
AV121657
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Pred. No. 1.4e-302;
); Mismatches 4;
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/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIOLYNR13"
/tissue type="Placenta Cot
/plasmid="pcMvSPORT_6"
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                                                                                BP141657
BP141351
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Homo sapiens
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Homo sapiens
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Best Local Similarity
Matches 949; Conserv
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VERSION
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 984)

1. (Dases 1 to 984)

1. (Dases 1 to 984)

1. (Dases 1 to 984)

2. Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

1. (Dupublished (2001)

On May 15, 2003 this sequence version replaced gi:30779500.

Contact: Genoscope

2. Tue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a /mod\_type="mRNA"
/db xref="taxon:9606"
/db xref="taxon:9606"
/clone="CSOCAP003YK21"
/clone\_Tib="Homo sapiens THYMUS"
/note="Vector: pcMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into Library was not normalized." 1265 1372 BX436692 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAP003YK21 5-PRIME, mRNA sequence. ä GTTCAACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGCGG 172 232 92 173 GITCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAG 1206 GTACCTACATTCTCTCCCTCCTTCTGCAAGGCTATCATTCACAGCTGATTCCTGGGAGG ACATCCATTTCATTGGCAAGATCCAGGGCAGCGACGCCGGCTGGACTTTGGGCTACATGC Gaps division of Invitrogen.
This sequence belongs to sequence cluster 5524.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOCAP003AF11QP1&c=5524.f.
Location/Qualifiers 1; Length 984; Indels 1253

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The FANTWM CONDSCILUM and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Lot 60,770 full-length cDNAs

E (bases 1 to 2410)

Adachi, J. Aizawa, K., Akimurra, T., Hara, A., Hashizume, W.,

Rukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,

Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, R., Ohno, M., Ohsato, N.,

Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakazume, N.,

Sano, H., Sasaki, C., Saitoh, R., Sakai, C., Sakazi, K., Sakazume, N.,

Sano, H., Sasaki, D., Saitoh, R., Shinagawa, A., Shiraki, T.,

Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,

Muramatsu, M. and Hayashizaki, Y.,

Direct Submission

Li Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, Kanagawa, 230-0045, Japan (E-mail:genome-reseasceriken.jp,

Kanagawa, 230-0045, Japan (E-mail:genome-reseasceriken.jp,

WEL:http://genome-gsc.riken.jp/, Tel:81-45-503-9212,
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   Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                               Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-langth to CDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
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                                                       cloning
                                    Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
9279253
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/mol_type="mRNA"
/strain="C57BL/6J"
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URL:http://fantom.gsc.riken.jp/
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Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:5330437E10 product:ectonucleoside triphosphate diphosphohydrolase 1, full insert sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                               --AGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAAGTTCTGTGCTCAGCCTTGGGAG
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                                                                                                        CTCAGGGACCCATGCTTTCATCCTGGATATAAGAAGGTAGTGACGTAAGTGACCTTTAC
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High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
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                                                                                                                         /note="unnamed protein product; ectonucleoside triphosphate diphosphohydrolase 1 (MGD|MGI:102805, GB|NM 009848, evidence: BLASTN, 100%, match=2284) putative"
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79.8%; Pred. No. 3.5e-243;
ive 0; Mismatches 255;
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Matches 1058; Conserv
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KYLAECMELSTELI PTSKHYOPVYLAATAGNELAKBESGABEVLAAVSTSLKSYP
PDFGGAK I I TGQTEEAYGM I I INYLLGRFTOBOSWLSL I SDSGKQETFGAL DLGGGAST
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79.8%; Pred. No. 4.3e-243;
ive 0; Mismatches 255;
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CONNAS

Nature 420, 563-573 (2002)

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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Haragaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Katoh, H., Kawai, J., Kolini, Y., Itoh, M., Kagwa, I., Kasukawa, T., Katoh, H., Kawai, J., Kolini, Y., Ishi, Y., Miyazaki, A., Mixata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                              Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshik, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_gfage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
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Nature 409, 685-690 (2001)
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Please visit our web site for further details.
URL:http://genome.gec.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                             Length 861;
                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                       56.5%; Score 812.4; DB 5; 99.2%; Pred. No. 2.3e-228; iive 0; Mismatches 3;
                                                           l. .861
/organism="Homo sapiens"
                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                857;
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMYSOPRT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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BX371889 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA CLONE CSODIO73YDO8 3-PRIME, mRNA sequence.
BX371889
BX371889. GI:46831287
                                                                                                                                                                                                                                                           101 TGCCCTTACTCCCAGTGTGCCTTCAATGGCGTCTTCCTGCCACCTCTCCATGGGAGTTTT 1160
                                                                                                                                                                                                                                                                                               GGGGCATTTTCAGCTTTTTACTTTGTGATGAAGTTTTTAAACTTGACATCAGAGAA---- 1133
                                                                                                                                                                                                                                                                                                                                11 6GGGCGTTTTCTGCTTTCTACTTTGTGATGGATTTTTTAAGAAGGTAGCGAAAACAGT 1220
                                                                                                                                                                                                                                                                                                                                                                                                     1221 GTCATCTCTCAGGAGAAATGACCGAGATAACAAAAATTTTTGCTCAAAATCTTGGGAA 1280
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                                                                                                              981 GGCACTCCCTGCACCAAAAGATTCGAAAAGAAGCTACCATTTGATCAGTTTCGAATCCAG 1040
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 861)
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                           CTTAAGGACCCATGCTTTAACCCAGGATACGAGAAGGTTGTGAATGTAAGTGAAGTCTAT
                                                                              898 AAGACCCCCTGCACCAAGAGATTTGAGATGACTCTTCCATTCCAGCAGTTTGAAATCCAG
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Full-length CDNA libraries and
Unpublished (2001)
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/protein_id="BAC26037.1"
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PSPCYGKDQALWOKLARKOIGVSGGAYLKDPCFNPGYERKVNNVSELYGTPCTRRFEKKL
PFDGFRIGGTGDYEGCHQSILELFNNSHCPYSQCAFNGVFLPPLHGSFGAFSAFYFVM
DFFKKYAKNSY 15.GEKOMTEITNRFCSKSWBETKTSYPSVKEKYLSEYCFSGAFYFVW
GGYNFTGSSWEGIHFWGKIKDSNAGWTLGYMLNLTNMIPAEQPLSPPLHSTYIGLMV
LFSLLLVAVAITGLFIYSKPSYFWKEAV."
                                                    Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp, Tel:81-45-503-9212, Pax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="skin"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                    cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     395
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                          The Institute of
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// inche="unnamed protein product; ectonucleoside
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                      Submitted (16-JUL-2001) Yoshihide Hayashizaki,
                                                                                                                                                                                                                                                                                                                                                                                                                  prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.7%; Score 743.4; DB 3;
79.2%; Pred. No. 9.8e-208;
iive 0; Mismatches 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
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3563 bp mRNA linear HTC 03-APR-2004
Mas musculus 10 days neonate skin cDNA, RIKEN full-length enriched
library, clone:473419419M16 product:ectonucleoside triphosphate
diphosphohydrolase 1, full insert sequence
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Pukuda, S., Puruno, M., Hanagaki, T., Hara, A., Hashizume, W.,

Fukuda, S., Puruno, M., Hanagaki, T., Hara, A., Hashizume, W.,

Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,

Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T.,

Katoh, H., Kawai, J., Kojima, Y., Kodo, S., Konno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,

Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,

Sano, H., Satashi, D., Shibata, K., Shinagawa, A., Shiraki, T.,

Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,

Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases I to 3563)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-langth to CDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                   AGCATCCTGGAGCTCTTCAACACC 1011
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSDORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db xref="taxon:9606"
/clone="CSODIO73YD09"
/tissue type="HACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NorI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
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                                                gi:31274964
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On F201 this sequence version replaced
Contact: Genoscope
Genoscope - Centre National de Sequencage
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 1014)

TCAGGAACAGAGTTGGCTAAGCCTCATCTCA---GACAGTCAGAAACAGGAAACCTTTGG
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Eukaryota sapiens
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 897)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31273939.
Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
                 305 GCGTGCTCAAGTAGAAGAAGAAGGATAAAGGTCCTGGAATCTCAAAATTTGTTC
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bulbasea 1 to 1066)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lu Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapba-r@mail.nih.gov
Tissue Procurement: Invitrogen

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

plate: LLANLST14 row: c column: 20

High quality sequence stop: 664.

Location/Qualifiers

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5', mRNA Sequence.
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Pred. No. 4.6e-203;
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Contact: Genoscope and Contact: Genoscope - Centre National de Sequencage
Z rue Gastono Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                            BX402316
BX402316 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI017YB13 5-PRIME, mRNA sequence.
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1. (bases 1 to 1025)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished (2001)

On May 13, 2003 this sequence version replaced gi:30610946.
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
                                               AAATTCTCAGGGACCCATGCTTTCATCCTGGATATAAGAAGGTAGTGAACGTAAGTGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 GCGTGGTGCATCAAGTAGAAGAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308 GCGTGGTGCATCAAGTAGAAGAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS1AI005ZB07QP1&c=5524.f. Location/Qualifiers
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Pred. No. 9.9e-196;
0; Mismatches 3;
                                                                                                                                        893 TTTACAAGACCCCTGCACCAAGAGATTTGA 923
                                                                                                                                                                                  867 TTWMAARMCCCCCCCMCMARARATTTARATGA 897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI017YB13"
                                                                                                                                                                                                                                                                                                                                                                                          BX402316.2 GI:46844926
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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  Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                                       /mol type="mixmo" diplome.
/mol type="mixmo" diplome.
/db xref="taxon:9606"
/clone="cS0D1059x011"
/tissue type="placexna cor 25-NORMALIZED"
/clone="list strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and BcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.1%; Score 720.6; DB 1; Length 897; 94.3%; Pred. No. 3.4e-201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Mismatches
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BX327984 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODIO73YD08 5-PRIME, mRNA sequence.
BX327984
BX327984.1 GI:30332721
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Homo sapiens
Homo sapiens
Bukaryotas, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
1 (bases 1 to 952)
Lidy Ma. (Stuber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                     GTTCTTCTCACACAAGTTTATACATCTATMAGTGGCCAGCAGAAAAAGGAGAATGACACAG
                                                                                                                                                                                               GCGTGGTGCATCAAGTAGAAGGTCCMGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC
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                                                                                                                                                                          GTTCAACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGCGG
                                                                                                                                                                                                                                                              GITCTICTCACACAAGTITATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAG
                                                                                                                                                                                                                                                                                                                                                GCGTGGTGCATCAAGTAGAAGAATGCAGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC
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                                                                                    48.5%; Score 697.6; DB 1; 98.6%; Pred. No. 2.3e-194; iive 5; Mismatches 5;
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Best Local Similarity 98.67
Matches 697; Conservative
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1 (base 1 to 1023)

2 Li, W. B., Gruber, C., Jessee, J. and Polayes, D.

3 Li, W. B., Gruber, C., Jessee, J. and Polayes, D.

4 Unpublished (2001)

5 Pull-length cDNA libraries and normalization

5 Londat: Genoscope

6 Contact: Genoscope

7 The 15, 2001 this sequence version replaced gi:31269551.

Contact: Genoscope

8 The 15 Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact: Contact:
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1023 bp mRNA linear EST 25-MAR-2004
4L547722 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
CLONE (SSDI017YB13 5-PRIME, mRNA sequence.
AL547722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /close="CSODIO177813"
/tissue type="PLACENTA COT 25-NORWALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/note="lst strand clopA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                              TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGACTTTGGACCTTGGGG
                                                                                                                               488 TGCTCAGGATGGAAAGTGAAAGAGTTGGAGGTTCTGGATGTGGAGAGGAGCC
                                                                                                                                                                                                                   TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGTG
                                        TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGAGGAGGCC
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/db_xref="taxon:9606"
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Homo sapiens
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/db_xref="taxon:9606"
/clone="IMAGE:5762493"
                                  1413 CACACCTCTCTCCCACTCCAC 1433
                                                    682 CACACCTGTCTTCCACTCCAC
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                                                                                                                                                                                                                                                              sapiens (human)
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nes 773; Conservative
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          Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequefe@genoscope.cns.fr, Web: www.genoscope.cns. Five prime
1st terrand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-errand cDNA was digested with Not i and clonec
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                                        /mol_type="maxx" | //mol_type="maxx" | //mol_type="maxx" | //mol_type="maxx" | //mol_type="maxx" | //mol_tiseue type="maxx" | //mole="lib="Homo sapiens PLACENTA COT 25-NORMALIZED" | //note="list strand cDNA was primed with a NotI-oligo(dT) | //mote="list strand cDNA was primed with notI and cloned into the NotI and cloned into the Not I and cloned into the Not I and cloned into the Not I and cloned into the Not I and coRNA sites of the pCMVSPORT 6 vector. Library was normalized."
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Pred. No. 2.6e-182;
0; Mismatches 8;
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6627603 NIH MGC_122 Homo sapiens CDNA clone IMAGE:5762493
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NIH-MGC http://wgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Londbulished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Biocesience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llhl.gov

Plate: LLAM12812 row: m column: 22

High quality sequence start: 4

High quality sequence start: 4

High quality sequence stop: 669.
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623 CTGGACTTTGGGCTACATGCTGAACCCTGACCACATGATCCCAGCTGAGCAACCATTGT- 681
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1061)
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/mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:4309819"
/tlssue type="primary B-cells from tonsils (cell line)"
/lab_host="IMAGE:48"
/clone=lib="MNHE MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: Xhol;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/Xhol sites using the blrectionally cloned into EcoR1/Xhol sites using the following 5' adaptor: GGACGAGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Pred. No. 6.6e-179;
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B. 1 (bases 1 to 808)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC.Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC.Clone distribution information can be http://image.llnl.gov

Plate: LLCM1183 row: n column: 16

High quality sequence stop; 758.
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    CTGGGCAAATTCAGTCAGAAACAAGGTGGTTCAGCATAGTCCCATATGAAACCAATAAT
                                                                     CAAAACCAGACTATCGAGTCCCCCAGATAATGCTCTGCAATTTCGCCTCTATGGCAAGGAC
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                                              CAGGAAACCTTTGGAGCTTTGGACCTTGGGGGGGGCCTCTACAAAGTCACTTTTGTACCC
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL COMMENT

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                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
1 (bases 1 to 673)
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Holzman,T.
                                                                                                                                                                                                                                                        University of Washington
Box 158070, Seattle, WA 98195-8070, USA
Tel: 206 732 6156
Fax: 206 732 6056
Email: ted@locke.hs.washington.edu
Similar to GenBank entry 873813 873813 CD39=lymphoid cell
activation antigen [human, B lymhpoblastoid cell line, MP-1, Plate: MMSP0076 row: A column: 03.
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    MMSP0076_A03 MMSP Macaca mulatta cDNA, mRNA sequence.
                                                                                                                                                                                         Expressed sequence tags from Rhesus macaque spleen Unpublished (2002)
Contact: Holzman T
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/db xref="taxon:9544"
/sex="male"
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Location/Qualifiers
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/dev_stage="adult"
/clone_lib="MMSP"
/note="Organ: spleen"
                                                             Macaca mulatta (rhesus monkey)
Macaca mulatta
                   CB553295
CB553295.1 GI:31302490
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Matches 662, Conservative
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VERSION
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        1204 TCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTTCTGGTACCTACATT
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        481 TCTTACGCTGGAGTAAAGGAAAGTCTGAGAGTGAATACTGCTTTTCTGGTACCTACATT
        540

        Db
        541 CTCTCCCTCTTCTGCAAGGCTATCA-TTTCACAGCTGATTCTGGGAGCACATCATT
        1323

        CTCTCCCTACTTCTGCAAGGCTATCA-TTTCACAGCTGATTCTGGGAGCACATCATT
        600

        Qy
        1323 CATTGGCAAGATCCAGGGCGACGCAGCGGGGCTACATTTGGGCTACATCTGTACATT
        600

        Qy
        1323 CATTGGCAAGATCCAGGGCGACGCGGGGCTACATGGGGAGCATCCTTT
        600

        Qy
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        Db
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        601 CAAAATGATCCC 1394

        Db
        661 CCAAAATGATCCC 673
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Search completed: September 21, 2005, 23:22:06 Job time : 5136.07 secs

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TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGAGCC 472
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Matches 1321; Conservative
TYPE: DNA
ORGANISM: Unknown
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LENGTH: 1818
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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Compugen Ltd.
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US-09-949-016-2106
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US-09-908-510A-3
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US-08-305-221-1
US-09-000-003A-1
                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters
                                                                                                                                                                                                                                1202784 seqs, 818138359 residues
            GenCore version
(c) 1993 - 2005
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                                                                                      September 21, 2005, 16:29:41
                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                   length: 0
length: 2000000000
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US-00-30-921-2

1 Sequence 2, Application US/08930921B

1 Sequence 2, Application US/08930921B

2 Sequence 2, Application US/08930921B

3 Sequence 2, Application US/08930921B

4 Sequence 2, Application US-08930921B

5 GENERAL INFORMATION:

APPLICANT: SEVIGNY, Jean

7 TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION

7 TITLE OF INVENTION: TECHNOLOGY

7 TITLE OF INVENTION: TECHNOLOGY

7 TITLE OF INVENTION: TECHNOLOGY

7 TITLE OF INVENTION: TECHNOLOGY

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7 TITLE OF INVENTION: TECHNOLOGY

7 TITLE OF INVENTION: TECHNOLOGY

7 TITLE OF INVENTION: TECHNOLOGY

7 TITLE OF INVENTION INPERS: POTOLOGY

7 TITLE OF INVENTION NUMBER: US/08/930,921B

7 CURRENT APPLICATION NUMBER: POTOLOGY

7 EARLIER PILING DATE: 1996-04-10

7 SOFTWARE: PATCHING UNCS: 8

7 SOFTWARE: PATCHING UNCS: 8

7 SOFTWARE: PATCHING UNCS: 8
                            Sequence 71597, A Sequence 1159, App Sequence 159, App Sequence 159, App Sequence 159, App Sequence 159, App Sequence 159, App Patent No. 5210029 Patent No. 5464939 Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Patent No. 5314995 Patent No. 5314995
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US-08-352-990-1

US-08-18-016-71597

US-08-18-009-159

US-08-46-156-1

US-08-46-736-159

US-09-46-736-159

US-09-663-67-159

US-09-663-67-159

US-09-663-67-159

US-09-61-159

US-09-61-159

US-09-61-159

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US-07-91-159

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99.8%; Pred. No. 0;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                            CONFUTER: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PErfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFCATION:
PRIOR APPLICATION:
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GENERAL 1475

Sequence 1475, Application US/09023655

Patent No. 667879

GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE
TITLE OF INVENTION: COMPOSITION FOR THE
TITLE OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-00:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1475:
SEQUENCE CHARACTERISTICS:
LENGTH: 1818 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
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APPLICATION NUMBER:
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; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9765255
US-09-023-655-1475
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CLASSIFICATION:
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                   TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGAAGGTG
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                                      GENERAL INCORMATION:
APPLICANT: BEAUDOIN, Adrien R.
APPLICANT: BEAUGOIN, Jean
APPLICANT: BEAUGOIN, Jean
APPLICANT: BACH, Fritz H.
APPLICANT: BACH, Fritz H.
APPLICANT: ROBSON, Simon
ITILE OF INVENTION: THEREOF AND PROCESS OF PROI
ITILE OF INVENTION: THEREOF AND PROCESS OF PROI
ITILE OF INVENTION: TECHNOLOGY
FILE REFERRENCE: 920333.90019
CURRENT APPLICATION NUMBER: US/09/781,796C
CURRENT APPLICATION NUMBER: 08/419,204
PRIOR APPLICATION NUMBER: 08/419,204
PRIOR FILING DATE: 1995-04-10
PRIOR FILING DATE: 1996-04-10
PRIOR FILING DATE: 1996-04-10
PRIOR FILING DATE: 1996-04-10
PRIOR FILING DATE: 1996-04-10
PRIOR FILING DATE: 1996-03-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PALENTIN VET: 2.1
SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                     91.8%; Score 1319.2;
99.8%; Pred. No. 0;
ive 0; Mismatches
Sequence 2, Application US/09781796C Patent No. 6800284 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 99.8 Matches 1321; Conservative
                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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is Sequence 5457, Application US/09949016
is Patent No. 681239
is GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
ITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
ITILE OF INVENTION: WIMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/02/141,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-03
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                                                                                                                                                                                                      198 GGTTGACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGCGG
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Pred. No. 7e-86;
0; Mismatches 575; Indels
                                                                                                                                   Indels
                                                                                     32.2%; Score 463.2; DB 4; 99.4%; Pred. No. 6.7e-144; iive 0; Mismatches 3;
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20.3%;
Best Local Similarity 54.3%;
Matches 707; Conservative
                                                                                                                                     465; Conservative
                                                                                         Query Match
Best Local Similarity
Matches 465; Conserv
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2106
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; ORGANISM: Human
US-09-949-016-5457
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; Bequence 2106, Application US/09949016
; Bettent No. 6812339
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR PELING DATE: 2000-10-03
; PRIOR PELING DATE: 2000-10-03
; PRIOR PELING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTHARE: PSELSEQ for Windows Version 4.0
; SEQ ID NO 2106
LENGTH: 871
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FREENT No. 6356477
GENERAL INFORMATION:
APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Anna-Maria
ITILE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
ITILE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
ITILE REPERENCE: 9598-066
CURRENT PELLING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 2797
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; LOCATION: (83)..(1669)
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; LENGTH: 2797
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
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US-09-908-510A-3
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FREEDER NO. 6759214
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: METHODS AND COMPOSITIONS
FILE REPERBNCE: 28110/36120E
CURRENT APPLICATION NUMBER: US/09/908,510A
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 09/240,639
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATCHIN VERSION 3.1
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                                                                                             GGGGGATTTTGGGGGCATTTTCAGCTTTTTACTTTGTGATGAAGTTTTTAAACTTGACATC
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                       Sequence 3, Application US/10107660
; Batent No. 6780977
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Chadwick, Brian Paul
; TITLE OF INVENTION: WETHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/10/107,660
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEO ID NOS: 29
; SOFTWARE: Patentin Ver. 2.0
; SEO ID NO 3
; LENGTH: 2797
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                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (83)..(1669)
US-10-107-660-3
                   US-10-107-660-3
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APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Brian Maria
APPLICANT: Frischauf, Anna Maria
APPLICANT: Frischauf, Anna Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND 1
TITLE OF INVENTION: ACIDS
FILE REFERENCE: 28110/36120H
CURRENT APPLICATION NUMBER: US/10/107,576
CURRENT FILING DATE: 2002-03-27
PRIOR FILING DATE: 1999-01-29
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US-10-107-576-3
, Sequence 3, Application US/10107576
, Patent No. 678359
, GENERAL INFORMATION:
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SEQ ID NO 3
LENGTH: 2797
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (83)..(1669)
CUSHINGORMATION:
US-10-107-576-3
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GENERAL INFORMATION:
APPLICANT: Chadwick, Brian Paul
APPLICANT: Chischauf, Anna Maria
APPLICANT: Crischauf, Anna Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
FILE REFERENCE: 28110/36120B
CURRENT APPLICATION NUMBER: 08/09/905,732B
CURRENT APPLICATION NUMBER: 09/240,639
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
NUMBER: OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
   TICTGGTACCTACATTCTCTCCTTCTGCAAGGCTATCATTCACAGCTGATTCCTG 1307
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                                                        GGAGGAGATAAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTT
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20.3%; Score 291; DB 4; Length 27
Best Local Similarity 54.3%; Pred. No. 7e-86;
Matches 707; Conservative 0; Mismatches 575; Indels
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; Patent No. 6787328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo Sapiens
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LOCATION: (83)
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US-09-905-732B-3
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 Score 291; DB 4; Length 2797;
Pred. No. 7e-86;
0; Mismatches 575; Indels 2
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al Similarity 54.3%;
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CURRENT APPLICATION NUMBER: US/09/923,304
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
FILE REFERENCE: UTSC:658US
                                                                     LENGTH: 2797
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                              .. (1672)
                                                                                                                                                                    Query Match
Best Local Similarity
Matches 707; Conserv
                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (83)
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                                                GGAGCACATCCATTTCATTGGCAAGATCCAGGGCAGCGACGCCGGCTGGACTTTGGGCTA
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                                                                                                AGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTTGGACCTTGGGGGGAGCCTTC
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APPLICANT: KATZ, RUTH APPLICANT: JIANG, FENG TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS

US-09-923-304-3 ; Sequence 3, Application US/09923304 ; Patent No. 6797471 ; GENERAL INFORMATION:

994 TGATAGCCTGTGCACTGTGGACCAGAAGGTTATAACCCCAATGATGTCATCAC 1053 5 179 239 719 779 836 279 339 459 419 519 639 669 629 753 813 GCATCAAGTAGAAGAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTCAGAAAGT 299 300 AAATGAAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGGGAAGTGATTCCAAG 359 GTTGCAAAATGAAACAGCAGCTAATGAAGTCCTTGAAAGCATCCAAAGCTACTTCAAGTC 579 720 ATTICGCCTCTATGGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGCTATGGGAA egigroccirciangecraceraracacercracacacacacriccaerecrangece GGATCAGGCACTCTGGCAGAAACTGGCCAAGGACATTCAGGTTGCAAGTAATGAAA---T GAATGAGGCTGAGAAGATTCTGGCAATGCTCCTGCAGAATTCTCCTACCAAAAACCA CTGGATTACTATCAACTATCTGCTGGCAAATTCAGTCAGAAAACAAGGTGGTTCAGCAT 700 gérec-----Accégcargeagregaaaccacederécecreeacrraderecre 180 TCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAGGCGTGGT ccaagargreeccagagecrirgaggagrerargeaaaagagggagggreare GATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGAGGCCTCAGCAA TCTCAGGGACCCATGCTTTCATCCTGGATATAAGAAGGTAGTGAACGTAAGTGACCTTTA 120 CCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGCGGGTTCTTC ccaccrccacearccaccccarrcaccressasccacescressarescristras 640 Aricchiracacccancrarrranicccanarrirccrccacaacaaccrcrccacarcrc 660 TACACAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATGCTCTGCA 754 cacccaaararcerregregeagagagagargaregarergaacaccagegacareargea GTCCCAGCACCAAGAGACACCCGTTTACCTGGGAGCCACGGCATGCGGTTGCTCAG CTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGAAGGTGCCTATGG Gaps 21; Length 2797; 0; Mismatches 575; Indels tch 20.3%; Score 291; DB 4; al Similarity 54.3%; Pred. No. 7e-86; 707; Conservative 0; Mismatches 575 837 934 ઠે В 8 8

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951 AATCCAGGGTATTGGAAACTATCAACAATGCCATCAAAGCATCCTGGAGCTCTTCAACAC 1010
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CAGTCAAACCTTCAAATGTAGTGTGAAAGGCTCTGGAAATCTCCAGCTATGGAAATAACCC 399
                                                      CCAAGATGTCCCCAGAGCCTTTGAGGAGTGTATGCAAAAAGTCAAGGGGCAGGTTCCATC 459
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                                                                                              AGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTGGGGGAGCCTC
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Sequence 178, Application US/09949016
Sequence 178, Application US/09949016
SENERAL INPORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF IFILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
SRIOR FILING DATE: 2000-10-03
SEQ ID NO SEQ ID NOS: 207012
SOFTWARE: F884SEQ for Windows Version 4.0
SEQ ID NO 1787
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Pred. No. 7e-86;
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Matches 707; Conservative
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ORGANISM: Human
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US-US-39 ULLELIBRAD

Sequence 13849, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PELICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRASESEQ for Windows Version 4.0

LENGTH: 46885
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54.3%; Pred. No. 7e-86;
iive 0; Mismatches 575; Indels
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APPLICANT: Chadwick, Anna Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS
TITLE OF INVENTION: METHODS AND COMPOSITIONS
FILE REFERENCE: 28110/36120C
CURRENT APPLICATION NUMBER: 08/09/905,743B
CURRENT FILING DATE: 12091-07-13
PRIOR APPLICATION NUMBER: 09/240,639
PRIOR APPLICATION NUMBER: 09/240,639
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3:1
                                                                                                                                                          Sequence 3, Application US/09905743B Patent No. 6828423 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (83)..(1669)
OTHER INFORMATION:
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Best Local Similarity
                                                                                                                         RESULT 14
US-09-905-743B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 3
LENGTH: 2797
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                                                                                   Score 270.2; DB 4; Length 46885;
Pred. No. 5.2e-78;
0; Mismatches 3; Indels 0;
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; TYPE: DNA
; CRCANISM: Human
; CRCANISM:
; NAME/KEY: misc_feature
; LOCATION: (1)...(46885)
; GTHER INFORMATION: n = A,T,C or G
US-09-949-016-13848
                                                                                  Query Match
Best Local Similarity 98.9%;
Matches 272; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Ouery No. Score Match Length DB ID Description

1 1437 100.0 1437 9 US-09-835-147-7 Sequence 7, Appli 3 1365 95.0 1365 9 US-09-835-147-5 Sequence 25, Appli 4 1319.2 91.8 1599 9 US-09-835-147-1 Sequence 1, Appli 5 1319.2 91.8 1818 18 US-10-646-308-29 Sequence 29, Appl 6 1319.2 91.8 1818 22 US-10-934-998-290 Sequence 290, Appl 7 1319.2 91.8 1818 22 US-10-934-998-290

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion
OTHER INFORMATION: construct of human CD39

8 1319.2 91.8 2081 22 US-10-934-998-46 9 1319.2 91.8 4411 16 US-10-204-998-191 10 640.2 44.6 6144 22 US-10-934-998-191 11 640.2 44.6 6144 22 US-10-934-998-191 12 414 28.8 475 10 US-0-918-995-24656 13 379 26.4 494 10 US-0-918-995-23056 13 379 26.4 494 10 US-0-918-995-23056 14 35.8 20.4 703 1 2797 20 US-0-918-995-23056 15 291 20.3 2797 22 US-10-934-998-191 18 270.2 18.8 374 16 US-10-09-386-23110 18 270.2 18.8 374 16 US-10-09-386-23110 20 260.8 18.1 1465 24 US-1-0-05-982-495 21 260.8 18.1 1465 24 US-1-0-05-982-495 22 199.2 13.9 2126 14 US-10-05-982-495 23 199.2 13.9 2126 14 US-10-175-737-495 25 199.2 13.9 2126 14 US-10-176-491-995 26 199.2 13.9 2126 14 US-10-176-915-495 27 199.2 13.9 2126 14 US-10-176-915-495 28 199.2 13.9 2126 14 US-10-176-915-495 29 199.2 13.9 2126 14 US-10-176-915-495 29 199.2 13.9 2126 14 US-10-176-915-495 29 199.2 13.9 2126 14 US-10-176-915-495 29 199.2 13.9 2126 14 US-10-176-915-495 29 199.2 13.9 2126 14 US-10-176-915-495 20 199.2 13.9 2126 14 US-10-176-915-495 21 199.2 13.9 2126 14 US-10-176-915-495 22 199.2 13.9 2126 14 US-10-176-915-495 23 199.2 13.9 2126 14 US-10-176-915-495 24 199.2 13.9 2126 14 US-10-176-915-495 25 199.2 13.9 2126 14 US-10-176-915-495 26 199.2 13.9 2126 14 US-10-176-915-495 27 199.2 13.9 2126 14 US-10-176-915-495 28 199.2 13.9 2126 14 US-10-176-915-495 28 199.2 13.9 2126 14 US-10-176-915-495 28 199.2 13.9 2126 14 US-10-176-915-495 28 199.2 13.9 2126 14 US-10-176-915-495 28 199.2 13.9 2126 14 US-10-176-915-495 28 199.2 13.9 2126 14 US-10-176-915-495 28 199.2 13.9 2126 14 US-10-176-915-495 28 199.2 13.9 2126 14 US-10-176-915-495 28 199.2 13.9 2126 14 US-10-176-915-495 28 199.2 13.9 2126 14 US-10-176-915-495 28 199.2 13.9 2126 14 US-10-176-915-495 28 199.2 13.9 2126 14 US-10-176-915-495 28 199.2 13.9 2126 14 US-10-176-916-495 28 199.2 13.9 2126 14 US-10-176-916-495 28 199.2 13.9 2126 14 US-10-176-916-495 28 199.2 13.9 2126 14 US-10-176-916-495 28 199.2 13.9 2126 14 US-10-176-916-495 28 199.2 13.9 2126 14 US-10-176-916-495 28 199.2 13.9 2126 14 US-10-176-916-495 28 199.2 1	Sequence 25 Sequen	Sequence 21, Appl Sequence 21, Appl Sequence 495, A	and Recruitment
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APPLICANT: Maliszewski, Charles R.
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Gayle III, Richard B.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE REFERENCE: 2879-US
CURRENT FILING DATE: 2001-04-13
FURRENT FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-06
PRIOR PLICATION NUMBER: US 60/107, 466
PRIOR PLICATION NUMBER: US 60/107, 466
PRIOR PLICATION NUMBER: US 60/107, 466
PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR PLICATION NUMBER: PCT/US99/22955
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NAME/KEY: CDS
LOCATION: (1).
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      ; NAME/KEY: CDS
; LOCATION: (1)..(1434)
US-09-835-147-7
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; Sequence 5, Application US/09835147
; Parent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Gayle III, Richard B.
APPLICANT: Gayle III, Richard B.
APPLICANT: Gimpel, Steven D.
: TITLE OF INVENTION: Inhibitors of Platelet Activation and Recr FILE REFERENCE: 2879-US
: CURRENT APPLICATION NUMBER: US/09/835,147
CURRENT FILING DATE: 2001-04-13
PRIOR PILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1999-11-06
; PRIOR FILING DATE: 1999-10-13
; PRIOR FILING DATE: 1999-10-13
; PRIOR FILING DATE: 1999-10-13
; RIOR PILING DATE: 1999-10-13
; RIOR PILING DATE: 1999-10-13
; RIOR PILING DATE: 1999-10-13
; RIOR PILING DATE: 1999-10-13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NOS: 31
; SEQ ID NOS: 31
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95.0%; Score 1365; D

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1365; Conservative 0; Mismatches
                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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; LOCATION: (1)..(1362)
US-09-835-147-5
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Patent No. US2002000227741

GENERAL INFORMATION:

APPLICANT: Majiszewski, Charles R.

APPLICANT: Gayle III, Richard B.

APPLICANT: Gayle III, Richard B.

APPLICANT: Gimpel, Steven D.

TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE REFERENCE: 2879-US

CURRENT APPLICATION NUMBER: US/09/835,147

CURRENT PILING DATE: 1989-10-16

PRIOR FILING DATE: 1998-11-06

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PRIOR FILING DATE: 1998-10-16

PRIOR FILING DATE: 1999-08-13

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PRIOR APPLICATION NUMBER: US 60/149,010

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PRIOR PILING DATE: 1999-08-13

PRIOR PILING DATE: 1999-08-13

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO II NO II NOS: 31
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ORGANISM: Homo sapiens
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TYPE: DNA
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE FILE REFERENCE: 3432-B
CURRENT PAPPLICATION NUMBER: US/10/646,308
CURRENT FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: --to be assigned--
PRIOR APPLICATION NUMBER: 60/406,418
PRIOR FILING DATE: 2003-08-12
PRIOR FILING DATE: 2003-08-28
NUMBER OF SEQ ID NOS: 36
SEQ ID NOS: 36
SEQ ID NO 29
LENGTH: 1599
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99.8%; Pred. No. 0;
ive 0; Mismatches
              NAME: Zeller, Karen J.
REGIGTRATION NUMBER: 37,071
REFERENCÉ/DOCKET NUMBER: PA-0001
TELECOMMUNICATION : NFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                    CLONE: 9765255
SEQUENCE DESCRIPTION: SEQ ID NO: 1475
                                                                                           TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1475:
SEQUENCE CHARACTERISTICS:
LENGTH: 1918 base pairs
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                      TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
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                                                    TTTACAAGACCCCCTGCACCAAGAGATTTGAGATGACTCTTCCATTCCAGGAGTTTGAAA
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 893 AAATTCTCAGGGACCCATGCTTTCATCCTGGATATAAGAAGGTAGTGAACGTAAGTGACC
                                  TTTACAAGACCCCCTGCACCAAGAGATTTGAGATGACTCTTCCATTCCAGCAGTTTGAAA
                                                                                               TCCAGGGTATTGGAAACTATCAACAATGCCATCAAAGCATCCTGGAGCTCTTCAACACCA
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Publication No. US20040077003A1
GENERAL INFORMATION:
Cocks, Benjamin G.
Sugan G. Stuart
Jeffrey J. Selihamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
GENERAL OF STRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
NNT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
FLASSIPICATION: UNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: «Unknown>
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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STATE: CALIFORNIA
COUNTRY: USA
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qq	894 AAATTCTCAGGGACCCATGCTTTCATCCTGGATATAAGAAGGTAGTGAACGTAAGTGACC 953	Query	/ Match 91.8%; Score 1319.2; DB 22; Length 1818;
ò	893 TITACAAGACCCCCTGCACCAAGAGATTTGAGATGACTCTTCCATTCCAGCAGTTTGAAA 952	Best Match	8 3; In
qq	954 TTTACAAGACCCCTGCACCAAGAGATTTGAGATGTCTTCCATTCCAGCAGTTTGAAA 1013	ò	113 GITCAACCCAGAACATIGCCACAAAACGITAAGIATIGIGAITIGIGGATIGGG 172
ò	953 TCCAGGGTATTGGAAACTATCAACAATGCCATCAAGCATCCTGGAGCTCTTCAACACCA 1012	qq	174 GGTTGACCCAGAACAAAGCGTTAAGTATGGGATTGTGTGTTTTTTTT
gg	1014 TCCAGGGTATTGGAAACTATCAACAATGCCATCAAAGCATCCTGGAGCTCTTCAACACCA 1073	ò	173 GITCITCTCACACATITATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACG 232
<u>ک</u> خ	1013 GTTACTGCCCTTACTCCCAGTGTGCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGG 1072	<b>д</b>	GTTCTTCTCTCACAAGTTTATACATCTATAAGTGGCCAGCAGCAGAAAGGAAATGACACA 2
}	ATTTTGGGGGGATTTTTGAGCTTTTTACTTTTGTGAAGATTTTTAAAGATTGAAGAAGATTTTAAAACTTGAAGAAGATTTTTAAAAGATTGAAGAAGATTTTTAAAAGATTGAAGAA	<b>è</b> €	233
g q		ìò	93 AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGGGAAGTGA 3
È	1133 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTGGGAGG 1192	qq	354 AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGGGAAGTGA 413
Db	1194 AGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAGTTCTGTGCTCAGCCTTGGGAGG 1253	ò	353 TTCCAAGGTCCCAGCACCCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGGCA
	AGATAAAAAACATCTTACGCTGGAGTAAAGGGAAGTACCTGAGTGAATACTGCTTTTCTG	qa	TTCCAAGGTCCCAGCACCAAGAGACACCCGTTTTACCTGGGAGCCACGCAGGCATGCGGT
	54 AGAIAAAAACAICIIIACGCIGGAGIAAAGGGGAGIACCIGAGIGAAIACIGCIIIICIG 53 CHAACAHAACAAHACAHAACAAHAAAAAAAAAAAAAAA	è t	TGCTCACGATGCAAAGTGAAGAKTTGGCAGAAAGGGTTCTGGATGTTGGTKGAGAKGAGGCC TGCTCACGATGTAAAAGTGAAAAAGAAATTGGCAGAAAGGGTTCTGGATGTTGGTKGAGAKGAGGCC
දු දු	1253 STACCTACATICTCTCTCTCTCTGCAAGGCTATCACAGCTGATTCCTGGGAAGC 1312 1314 GTACCTACATTCTCTCCCTCCTTCTGCAAGCTGATTCCTGGGAACC 1373	8 &	474 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGAGTTCTGGATGTGGGGGAGGAGGAGGACC 533
	ACATCCATTTCATTGGCAAGATCCAGGGCAGCGACGGCCGGC	6 Q	TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGAAGGTG
Db	1374 ACATCCATTTCATTGGCAAGATCCAGGGAGGCACGCCGGCTGGACTTTGGGCTACATGC 1433	ò	533 CCTATGGCTCGGATTACTATCTACTACTGCTGGGCAATTCAGTCAG
ò	1373 TGAACCTGACCAACAAGATCCCAGCTGAGCAACCATTGTCCACACTCTCTCCCACTCCA 1432	qq	S94 CCTATGGCTGGATTACTATCTATCTGCTGGGCAATTCAGTCAG
Dp	1434 TGAACCTGACCAACATGATCCCAGCTGAGCAACCATTGTCCACGTCTCTCCCCACTCTC 1493	ò	593 TCAGCAIAGTCCCATAIGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 652
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	1494 CCTA 1497	oy G	653 GAGCCTCTACAAGTCACTTTTGTACCCAAAACCAGACTATCGAGTCCCCAGATAATG 712
RESULT 7 US-10-934 ; Sequency ; Publica	RESULT 7 US-10-934-998-290 ; Sequence 290, Application US/10934998 ; Publication No. US20050153917Al	Qy Dp	713 CTCTGCAATTTCGCCTCTATGGCAAGACTACAATGTCTACACACATAGCTTCTTGTGCT 772
GENERAL  APPLIC  APPLIC  APPLIC	L INFORMATION: CANT: AL-MAHMOOD, SALMAN SANT: COLIN, SYLVIE	ે જ	ATGGGAAGGATCAGGCACTCCGCAGAAACTGGCCAAGGACACTTCAGGTTGCAAGTAATG
; TITLE	OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF	3 8	833 AAATTCTCAGGGACCCATGCTTTCATCCTGGATATAAGAAGGTAGTGAGGTAGTAAGTGACCTAAGTGACG
; FILE R	REFERENCE: BMA-04-1206 TA APPLICATION NUMBER: US/10/934,998	අු	
PRIOR	A FILING DATE: 2004-03-03-03-04-03-03-04-03-03-03-03-03-03-03-03-03-03-03-03-03-	ò	93 TTTACAAGACCCCTGCACCAAGAGATTTGAGATGACTCTTCCATTCCAGCAGTTTGAAA
PRIOR	APPLICATION NUMBER: FR02/02717 FILING DATE: 2002-03-04	අු	
; PRIOR ; PRIOR ; NUMBER	; PRIOR APPLICATION NUMBER: PR02/04546 ; PRIOR FILING DATE: 2002-04-11 ; NUMBER OF SEQ ID NOS: 301	<b>ራ</b> 8	953 TCCAGGGTATTGGAAACTATCAACAATGCCATCAAAGCATCCTGGAGCTCTTCAACCA 1012
SOFTWA	ARE: PatentIn version 3.2 NO 290	ò	1013 GTFACTGCCCTTACTCCCAGTGTGCCTTCAATGGGATTTTTCTTGCCACCACTCCAGGGG 1072
; LENGT ; TYPE:	; LENGTH; 1818 ; TYPE: DNA ; ORGANISM: Home ganiens	qq	1074 GTTACTGCCCTTACTCCCAGTGTGCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGG 1133
PUBLIC	CATION INFORMATION: BASE ACCESSION NUMBER: Genbank/S73813	ò	1073 ATTTTGGGGCATTTTCAGCTTTTTACTTTGTGATGAGTTTTTAAACTTGACATCAGAGA 1132
, DATAB US-10-934	DATABASE ENTRY DATE: 1995-04-12 -10-934-998-290	අු	ATTTTGGGGCATTTTCAGCTTTTTTACTTTGTGATGAGTTTTTAAACTTGACATCAGAGA
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              TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGAAGGTG
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Publication No. US20050153917A1

GENERAL INFORMATION:

APPLICANT: AL-MAHMOOD, SALMAN

APPLICANT: CCLIN, SYLVIE

APPLICANT: CCLIN, SYLVIE

TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL

TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF

FILE REFERENCE: BMA-04-1206

CURRENT APPLICATION NUMBER: US/10/934,998

CURRENT APPLICATION NUMBER: PCT/FR03/00695

PRIOR APPLICATION NUMBER: PCT/FR03/00695

PRIOR FILING DATE: 2003-03-04

PRIOR FILING DATE: 2002-03-04

PRIOR FILING DATE: 2002-04-11

NUMBER OF SEQ ID NOS: 301

NUMBER OF SEQ ID NOS: 301

LENGTH: 2081
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                                                                                         GTACCTACATTCTCTCCCTCCTTCTGCAAGGCTATCATTTCACAGCTGATTCCTGGGAGC 1312
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AGATAAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTTCTG
                                                      1254 AGATAAAAAACATCTTACGCTGGAGTAAAAGGAGAAGTACCTGAGTGAATACTGCTTTTCTG
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DATABASE ENTRY DATE: 2000-01-19
RELEVANT RESIDUES: (1)..(2081)
US-10-934-998-46
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Best Local Similarity 99.8%;
Matches 1321; Conservative (
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ORGANISM: Homo sapiens
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; GENERAL INFORMATION:
APPLICANT: AL-WAHMOOD, SALMAN
; APPLICANT: COLIN, SYLVIE
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APPLICANT: SHIFFMAN, DOV
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APPLICANT: SHIFFMAN, DOV
APPLICANT: SOMGYTI, Roland
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APPLICANT: SOMGYTI, Roland
APPLICANT: PORTER, Gordon J.
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91.8%; Score 1319.2;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1321; Conservative 0; Mismatches
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OTHER INFORMATION: a, t, c, g, or other
                                                                                                                                                                                                  Sequence 242, Application US/10240965
Publication No. US20030165924A1
GENERAL INFORMATION:
                                                           CCTA 1436
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APPLICANT: SCHNEIDER, CHRISTOPHE
TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL
TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF
FILE REFERENCE: BMA-04-1206
CURRENT APPLICATION NUMBER: US/10/934,998
CURRENT FILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: PCT/FR03/00695
PRIOR APPLICATION NUMBER: FR02/02717
PRIOR FILING DATE: 2002-03-03-04-09
PRIOR PILING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PATCHIN VERSION 3.2
SEQ ID NO 147
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44.6%; Score 640.2; DB 22; Length 704;
Best Local Similarity 99.5%; Pred. No. 1.6e-192;
Matches 642; Conservative 0; Mismatches 3; Indels 0;
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CORGANISM: Homo sapiens
US-10-934-998-147
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US-10-934-998-193/c
; Sequence 193, Appli
; Publication No. US2
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APPLICANT: AL-MAHMOOD, SALMAN
APPLICANT: AL-MAHMOOD, SALMAN
APPLICANT: AL-MAHMOOD, SALMAN
APPLICANT: AL-MAHMOOD, SALMAN
APPLICANT: COLIN. SYLVIE
APPLICANT: COLIN. SYLVIE
TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL
TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF
TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF
CURRENT APPLICATION NUMBER: US 1004-09-03
PRIOR APPLICATION NUMBER: FR02/0217
PRIOR PILLING DATE: 2003-03-04
PRIOR FILLING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PATCHING VERSION 3.2
SEQ ID NO 193
LENGTH: 6164
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Matches 642; Conserv
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RESULT

Sequence 193, Application US/10934998 Publication No. US20050153917A1

Gaps

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Length 484;

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CTTTCGGCTACATGCTGAACCTGACCACATGATCCCAGCTGAGCAACCATGTCCACAC 1417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Sequence 275, Application US/10002631C |
| Publication No. US20030157486A1 |
| GENERAL INFORMATION: |
| APPLICANT: Graff, Jonathon M. |
| APPLICANT: Muenster, Matthew |
| TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES |
| FILE REPRENCE: A34943 090495,0243 |
| CURRENT APPLICATION NUMBER: US/10/002,631C |
| CURRENT FILING DATE: 2001-10-31 |
| PRIOR APPLICATION NUMBER: 60/300,309 |
| PRIOR FILING DATE: 2001-6-21 |
| NUMBER OF SEQ ID NOS: 324 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 275 |
                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                       Query Match
26.4%; Score 379; DB 10; L
Best Local Similarity 100.0%; Pred. No. 2.1e-109;
Matches 379; Conservative 0; Mismatches 0;
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                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(484)
COTHER INFORMATION: n = A,T,C or G
US-09-918-995-23052
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; NAME/KEY: unsure
; LOCATION: (656)...(698)
; OTHER INFORMATION: n = A, C, US-10-002-631C-275
                            TYPE: DNA
ORGANISM: Homo sapiens
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            Sequence 24656, Application US/09918995
Publication No. US20030073623A1
GENERAL INCORMATION:
APPLICANT: Hyeseq. Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/918,995
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTHARE: FRABESEQ FOR WINDOWS VERSION 3.0
SEQ ID NO 24656
LENGTH: 475
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; Sequence 20052, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyeaq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/215,076
; PRIOR APPLICATION NUMBER: US/09/225,076
; PRIOR APPLICATION NUMBER: US/09/225,076
; NUMBER OF FOLING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SCOTWARR: FastSEQ for Windows Version 3.0
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Matches 423; Conservative
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US-09-918-995-24656
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                                                                                                     GTGCATCAAGTAGAAGAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTCAGAAA
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                                     TCTCACACACAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAGGCGTG
                                                                                                                                                                                               367 ACAGATGAAATCGGTGCGTACCTGGCCGAATGCATGGAACTGTCCACCGAACTGATACCA
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Pred. No. 7e-81;
0; Mismatches 575; Indels
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Patent No. US20020081612A1
GENERAL INFORMATION:
APPLICANT: KATZ, RUTH
APPLICANT: JANG, FENG
TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMO;
FILE REFERENCE: UTSC:658US
CURRENT APPLICATION NUMBER: US/09/923,304
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver: 2.1
SOFTWARE: Patentin Ver: 2.1
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Best Local Similarity 54.3%;
Matches 707; Conservative (
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ORGANISM: Homo sapiens
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, LOCATION: (83)..(1672)
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US-09-923-304-3
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